

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 13:52:13 ; Search time 7671 Seconds
(without alignments)
4649.073 Million cell updates/sec

Title: US-10-075-105C-1

Perfect score: 736

Sequence: 1 ggatccagcgtgtctctcc.....ggagaggacacgtgtgatcc 736

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_ats.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554	75.3	661	6	I06305 Sequence 34
2	554	75.3	661	6	I07318 Sequence 30
3	554	75.3	2107	6	AR229556 Sequence
4	554	75.3	2122	6	AR229554 Sequence
5	554	75.3	2436	6	AR229557 Sequence
6	554	75.3	3469	6	AR271023 Sequence
7	554	75.3	3754	6	AR271019 Sequence
8	554	75.3	8012	6	AR143709 Sequence
9	554	75.3	8012	6	BD008400 Glycosat
10	554	75.3	8349	6	AR260588 Sequence
11	554	75.3	8418	6	AR143713 Sequence
12	554	75.3	8418	6	BD008404 Glycosat
13	554	75.3	8798	6	AR143712 Sequence
14	554	75.3	8798	6	BD008403 Glycosat
15	552.4	75.1	661	6	BD013916 Vermin da
16	551.4	74.9	1030	6	AR003011 Sequence
17	551.4	74.9	5796	6	AX151106 Sequence
18	551.4	74.9	5897	6	BD132716 Regulator
19	551.4	74.9	5897	6	AR209019 Sequence

20	551.4	74.9	5897	6	AR482088 Sequence
c 21	551.4	74.9	9361	6	BD251965 Artificialia
c 22	551.4	74.9	10629	6	BD251966 Artificialia
23	550.4	74.8	9335	6	BD132709 Regulator
24	550.4	74.8	9335	6	AR209012 Sequence
25	550.4	74.8	9335	6	AR482081 Sequence
26	550	74.7	10249	6	AR260586 Sequence
27	550	74.7	10339	6	AR260585 Sequence
28	548.4	74.5	10160	6	BD132698 Regulator
29	548.4	74.5	10160	6	AR209001 Sequence
30	548.4	74.5	10160	6	AR482070 Sequence
31	548.4	74.5	11784	6	BD132699 Regulator
32	548.4	74.5	11784	6	AR209002 Sequence
33	548.4	74.5	11784	6	AR482071 Sequence
34	548.4	74.5	11991	6	BD132700 Regulator
35	548.4	74.5	11991	6	AR209003 Sequence
36	548.4	74.5	11991	6	AR482072 Sequence
37	543.6	73.9	4149	6	AR271018 Sequence
38	534.6	72.6	5767	6	AX275254 Sequence
39	534.6	72.6	14446	6	AX275255 Sequence
c 40	526	71.5	8626	12	CVU10459 Binary clon
c 41	526	71.5	8626	12	CVU10488 Binary clon
c 42	526	71.5	8731	12	CVU10463 Binary clon
c 43	526	71.5	8731	12	CVU10491 Binary clon
c 44	526	71.5	8909	12	CVU10458 Binary clon
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ALIGNMENTS

RESULT 1
LOCUS I06305 661 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 34 from Patent EP 0289479.
ACCESSION I06305
VERSION I06305.1 GI:590686
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 661)
AUTHORS Fischhoff,D.A., Fuchs,R.L., McPherson,S.A., Lavrik,P.B. and Perlak,F.J.
TITLE Insect-resistant plants
JOURNAL Patent: EP 0289479-A2 34 02-NOV-1988;
FEATURES Location/Qualifiers
source
1..661
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN	Query Match	75.3%	Score 554;	DB 6;	Length 661;
	Best Local Similarity	94.5%	Pred. No. 2.5e-163;		
	Matches 586;	Conservative 0;	Mismatches 30;	Indels 4;	Gaps 1;
Qy	116	TCTCAGTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCCTCGGATTCATTGCC	175		
Db	20	TCCGATGTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCCTCGGATTCATTGCC	79		
Qy	176	CAGTATCTGTCTACTTCATCAAAAGGACAGTAGAAAAGGAGGTGGGACCTACAAATGCC	235		
Db	80	CAGTATCTGTCTACTTTTATTTGTGAAGATAGTGGAAAAGGAGGTGGTCTCTACAAATGCC	139		
Qy	236	ATCATTCGATAAAGGAAAGGCTATCGTTCAGATGCTCTGCCGACAGTGGTCCCAAG	295		
Db	140	ATCATTCGATAAAGGAAAGGCTATCGTTCAGATGCTCTGCCGACAGTGGTCCCAAG	199		
Qy	296	ATGACCCCCCACCACCGAGGAGCATCGTGGAAAAGACGTTTCCAAACACGCTTTCAA	355		
Db	200	ATGGACCCCCCACCACCGAGGAGCATCGTGGAAAAGACGTTTCCAAACACGCTTTCAA	259		
Qy	356	AGCAAGTGGATTGATGTGAT-----TGCAGTGAGACTTTTCAACAAGGGTAATATCGGGA	411		

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50

32 TCTGCCGACAGTGGTCCC

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Db      448  TCTGCCGACAGTGGTCCAAAAGATGGACCCACCACGAGGAGCATCGTGGAAAAAGAA 507
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Db      508  GAGCTTCCACCAGCTTTCAAGCAAGTGGATGTGATATCTCCATCGACGTAAGG 567
Qy      652  GATGACGCACAATCCCACTATCTTCCGAAGACCTTCTCTATATAGGAAGTTCATTT 711
Db      568  GATGACGCACAATCCCACTATCTTCCGAAGACCTTCTCTATATAGGAAGTTCATTT 627
Qy      712  CATTTGGAGAGGACACGCTG 731
Db      628  CATTTGGAGAGGACACGCTG 647

RESULT 6
LOCUS   AR271023              3469 bp      DNA      linear      PAT 10-APR-2003
DEFINITION
Sequence 23 from patent US 6501009.
ACCESSION AR271023
VERSION   AR271023.1 GI:29702289
KEYWORDS
SOURCE   Unknown.
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 3469)
AUTHORS  Romano, C.P.
TITLE    Expression of Cry3B insecticidal protein in plants
JOURNAL  Patent: US 6501009-A 23 31-DEC-2002;
FEATURES
source   1..3469
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ORIGIN
Query Match 75.3%; Score 554; DB 6; Length 3469;
Best Local Similarity 94.5%; Pred. No. 2.7e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy      116  TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 175
Db      28  TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 87
Qy      176  CAGCTATCTGTCACTTTCATCAAAAGGACGTAGAAAAGAGGTGGCACCTACAAATGCC 235
Db      88  CAGCTATCTGTCACTTTCATCAAAAGGACGTAGAAAAGAGGTGGCTCTTACAAATGCC 147
Qy      236  ATCATTCGGATAAAGGAAGGCTATCGTTCAAGATCGCTCTGCCGACAGTGGTCCCAAAG 295
Db      148  ATCATTCGGATAAAGGAAGGCTATCGTTCAAGATCGCTCTGCCGACAGTGGTCCCAAAG 207
Qy      296  ATGGACCCCAACCCACGAGGAGCATCGTGGAAAAGAGACGTTCCCAACACGCTCTTCAA 355
Db      208  ATGGACCCCAACCCACGAGGAGCATCGTGGAAAAGAGACGTTCCCAACACGCTCTTCAA 267
Qy      356  AGCAAGTGGATTGATGTGAT- - - - -TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db      268  AGCAAGTGGATTGATGTGATGTGTCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 327
Qy      412  AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
Db      328  AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTATTTGTGAAGATAGTGGAAAAG 387
Qy      472  GAAGTGGGACCTTCAATGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 531
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Qy      472  GAAGTGGGACCTTCAATGCCAGCTATTCGGATAAAGGAAGGCTATCGTTCAAGATGCC 531
Db      388  GAAGTGGGCTCTTCAAAATGCCATCATTTGGGATAAAGGAAGGCCATCGTTGAAGATGCC 447
Qy      532  TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 591
Db      448  TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 507
Qy      592  GAGCTTCCAAACAGCTTTCAAGCAAGTGGATGTGATATCTCCATCGACGTAAGG 651
Db      508  GAGCTTCCAAACAGCTTTCAAGCAAGTGGATGTGATATCTCCATCGACGTAAGG 567
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Db      508  GAGCTTCCAAACAGCTTTCAAGCAAGTGGATGTGATATCTCCATCGACGTAAGG 567
Qy      652  GATGACGCACAATCCCACTATCTTCCGAAGACCTTCTCTATATAGGAAGTTCATTT 711
Db      568  GATGACGCACAATCCCACTATCTTCCGAAGACCTTCTCTATATAGGAAGTTCATTT 627
Qy      712  CATTTGGAGAGGACACGCTG 731
Db      628  CATTTGGAGAGGACACGCTG 647

RESULT 7
LOCUS   AR271019              3754 bp      DNA      linear      PAT 10-APR-2003
DEFINITION
Sequence 15 from patent US 6501009.
ACCESSION AR271019
VERSION   AR271019.1 GI:29702285
KEYWORDS
SOURCE   Unknown.
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 3754)
AUTHORS  Romano, C.P.
TITLE    Expression of Cry3B insecticidal protein in plants
JOURNAL  Patent: US 6501009-A 15 31-DEC-2002;
FEATURES
source   1..3754
/mol_type="genomic DNA"

ORIGIN
Query Match 75.3%; Score 554; DB 6; Length 3754;
Best Local Similarity 94.5%; Pred. No. 2.7e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy      116  TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 175
Db      28  TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCTCGGATTCATTTGCC 87
Qy      176  CAGCTATCTGTCACTTTCATCAAAAGGACGTAGAAAAGAGGTGGCACCTACAAATGCC 235
Db      88  CAGCTATCTGTCACTTTCATCAAAAGGACGTAGAAAAGAGGTGGCTCTTACAAATGCC 147
Qy      236  ATCATTCGGATAAAGGAAGGCTATCGTTCAAGATCGCTCTGCCGACAGTGGTCCCAAAG 295
Db      148  ATCATTCGGATAAAGGAAGGCTATCGTTCAAGATCGCTCTGCCGACAGTGGTCCCAAAG 207
Qy      296  ATGGACCCCAACCCACGAGGAGCATCGTGGAAAAGAGACGTTCCCAACACGCTCTTCAA 355
Db      208  ATGGACCCCAACCCACGAGGAGCATCGTGGAAAAGAGACGTTCCCAACACGCTCTTCAA 267
Qy      356  AGCAAGTGGATTGATGTGAT- - - - -TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db      268  AGCAAGTGGATTGATGTGATGTGTCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 327
Qy      412  AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
Db      328  AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTATTTGTGAAGATAGTGGAAAAG 387
Qy      472  GAAGTGGGACCTTCAAAATGCCAGCTATTCGGATAAAGGAAGGCTATCGTTCAAGATGCC 531
Db      388  GAAGTGGGCTCTTCAAAATGCCATCATTTGGGATAAAGGAAGGCCATCGTTGAAGATGCC 447
Qy      532  TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 591
Db      448  TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 507
Qy      592  GAGCTTCCAAACAGCTTTCAAGCAAGTGGATGTGATATCTCCATCGACGTAAGG 651
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Qy      652  GATGACGCACAATCCCACTATCTTCCGAAGACCTTCTCTATATAGGAAGTTCATTT 711
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Qy 712 CATTGGAGGACACGCTG 731
Db 3623 CATTGGAGGACACGCTG 3642

RESULT 12
BD008404
LOCUS BD008404 8418 bp DNA linear PAT 31-JAN-2002
DEFINITION Glycosate resistant transgenic plants.
ACCESSION BD008404
VERSION BD008404.1 GI:18636777
KEYWORDS JP 2001503280-A/5.
SOURCE unclassified
ORGANISM unclassified.

REFERENCE
1 (bases 1 to 8418)
Mannerloef, M., Tenning, P. P. and Steen, P.
Glycosate resistant transgenic plants
Patent: JP 2001503280-A 5 13-MAR-2001;
NOVARTIS AG
OS Unidentified
PN JP 2001503280-A/5
PD 13-MAR-2001
PF 29-OCT-1998 JP 1999525342
PI 31-OCT-1997 US 60/112003
PI MARIE MANNERLOEF, PAUL PETER TENNING, PER STEEN PC
C12N15/82, A01H5/00, A01H5/10
CC Strandedness: Double;
CC Topology: Linear;
CC Key Location/Qualifiers
FT source 1..8418
FT 1.8418
FT Location/Qualifiers
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ORIGIN
Query Match 75.3%; Score 554; DB 6; Length 8418;
Best Local Similarity 94.5%; Pred. No. 2.8e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCGATGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
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Qy 236 ATCATTCGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAG 295
Db 3143 ATCATTCGGATAAAGGAAGGCTATCGTTGAAGATGCTCTGCCGACAGTGGTCCCAAG 3202

Qy 296 ATGACACCCCAACCCAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACACGCTTTCAA 355
Db 3203 ATGACACCCCAACCCAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACACGCTTTCAA 3262

Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 3263 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 3322

Qy 412 AACCTCTCGATTCCCATTCGCGAGCTATCTGTCACTTCAATCAAAAGGACAGTAGAAG 471
Db 3323 AACCTCTCGATTCCCATTCGCGAGCTATCTGTCACTTTATTTGTGAAGATAGTGGAAAAAG 3382

Qy 472 GAAGTGGCACTTACAAATGTCATTCATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCC 531
Db 3383 GAAGTGGCTCTTACAAATGTCATTCATTCGGATAAAGGAAAGGCTATCGTTGAAGATGCC 3442

Qy 532 TCTCCGACAGTGGTCCCAAGATGGACCCCAACCCAGGAGGATCGTGGAAAAAGAA 591

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Qy 592 GAGTTCCTCAACACGCTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 3192
Db 3503 GAGTTCCTCAACACGCTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 3252
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Qy 712 CATTGGAGGACACGCTG 731
Db 3623 CATTGGAGGACACGCTG 3642

RESULT 13
AR143712
LOCUS AR143712 8798 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6204436.
ACCESSION AR143712
VERSION AR143712.1 GI:15104998
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 8798)
AUTHORS Mannerloef, M., Tenning, P. Peter. and Steen, P.
TITLE Transgenic plants
JOURNAL Patent: US 6204436-A 4 20-MAR-2001;
FEATURES
source 1..8798
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ORIGIN
Query Match 75.3%; Score 554; DB 6; Length 8798;
Best Local Similarity 94.5%; Pred. No. 2.8e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCGATGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 3133 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 3192

Qy 176 CAGCTATCTGTCATCTTCAACAAAGGACAGTAGAGAAAGGAGGTGGCACTTACAAATGCC 235
Db 3193 CAGCTATCTGTCATCTTATTTGTGAGATAGTGGAAAGGAGGTGGCTCTTACAAATGCC 3252

Qy 236 ATCATTCGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAG 295
Db 3253 ATCATTCGGATAAAGGAAGGCTATCGTTGAAGATGCTCTGCCGACAGTGGTCCCAAG 3312

Qy 296 ATGACACCCCAACCCAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACACGCTTTCAA 355
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Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 3373 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 3432

Qy 412 AACCTCTCGATTCCCATTCGCGAGCTATCTGTCACTTCAATCAAAAGGACAGTAGAAG 471
Db 3433 AACCTCTCGATTCCCATTCGCGAGCTATCTGTCACTTTATTTGTGAAGATAGTGGAAAAAG 3492

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Db 3553 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCAGGAGGATCGTGGAAAAAGAA 3612

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Qy 712 CATTTGGAGGAGCACGCTG 731
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RESULT 14
BD008403 8798 bp DNA linear PAT 31-JAN-2002
DEFINITION Glyposate resistant transgenic plants.
ACCESSION BD008403
VERSION BD008403.1 GI:18636776
KEYWORDS JP 2001503280-A/4.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 8798)
AUTHORS Mannerloef,M., Tennig,P.P. and Steen,P.
TITLE Glyposate resistant transgenic plants
JOURNAL Patent: JP 2001503280-A 4 13-MAR-2001;
NOVARTIS AG
COMMENT OS Unidentified
PN JP 2001503280-A/4
PD 13-MAR-2001
PF 29-OCT-1998 JP 1999525342
PI 31-OCT-1997 US 60/112003
PL MARIE MANNERLOEF,PAUL PETER TENNING,PER STEEN PC
CL2N15/82,A01H5/00,A01H5/10
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..8798
FT /organism='Unidentified'.
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source
1..8798
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

ORIGIN

Query Match 75.3%; Score 554; DB 6; Length 8798;
Best Local Similarity 94.5%; Pred. No. 2.8e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGCACTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 175
Db 3133 TCGATGTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 3192
Qy 176 CAGCTATCTGCTACTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGCCACTACAAATGCC 235
Db 3193 CAGCTATCTGCTACTTTATTGTGAAGATAGTGAAGAGGAGGTGGCTCTACAAATGCC 3252
Qy 236 ATCATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGCAAGTGGTCCCAAAG 295
Db 3253 ATCATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGCAAGTGGTCCCAAAG 3312
Qy 296 ATGACCCCCCACCACGAGGAGATCGTGGAAAAGAGACGTTCCAAACCACTCTTCAA 355
Db 3313 ATGACCCCCCACCACGAGGAGATCGTGGAAAAGAGACGTTCCAAACCACTCTTCAA 3372
Qy 356 AGCAAGTGGATTGATGTGAT- - - -TGCACTGAGACTTTTCAACAAGGGTAATATCGGGA 411
Db 3373 AGCAAGTGGATTGATGTGATGCTCGGATGTGAGACTTTTCAACAAGGGTAATATCGGGA 3432
Qy 412 AACCTCTCGGATTCGATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
Db 3433 AACCTCTCGGATTCGATTCGCCAGCTATCTGTCACTTTTATTGTGAAGATAGTGGAAAAG 3492
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Qy 472 GAGGTGGCACCTTACAAATGCCATCTTCCGATAAAGGAAAGGCTATCGTTCAAGATGCC 531
Db 3493 GAAGTGGGTCTCTTACAAATGCCATCTTCCGATAAAGGAAAGGCTATCGTTGAAGATGCC 3552
Qy 532 TCTGCCGACAGTGGTCCCAAGATGACCCCAACCCACGAGGAGCATCGTGGAAAAGAA 591
Db 3553 TCTGCCGACAGTGGTCCCAAGATGACCCCAACCCACGAGGAGCATCGTGGAAAAGAA 3612
Qy 592 GAGTTTCCAAACCAAGTGGTTCCTTCAAGCAAGTGGATGATGTGATATCTCCACTGACGTAAGG 651
Db 3613 GAGTTTCCAAACCAAGTGGTTCCTTCAAGCAAGTGGATGATGTGATATCTCCACTGACGTAAGG 3672
Qy 652 GATGACGCAACTCCCACTATCTTCCGCAAGACCTTCTCTATATAAGGAAGTTCATTT 711
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Db 3733 CATTTGGAGGAGCACGCTG 3752

RESULT 15
BD013916
LOCUS BD013916
DEFINITION Vermin damage-resistant plant.
ACCESSION BD013916
VERSION BD013916.1 GI:22554245
KEYWORDS JP 2001112490-A/19.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 661)
AUTHORS Fiskehof,D.A., Fuchs,R.L., Labrik,P.B., Mcpherson,S.A. and
Perlak,F.J.
TITLE Vermin damage-resistant plant
JOURNAL Patent: JP 2001112490-A 19 24-APR-2001;
MONSANTO CO
COMMENT OS Unidentified
PN JP 2001112490-A/19
PD 24-APR-2001
PF 07-SEP-2000 JP 2000272128
PR 29-APR-1987 US 044081
PI DAVID ALLEN FISKEHOF,ROY LEE FUCHS,PAUL BRUNO LABRIK PI
SYLVIA ANNE MCPHERSON,
PI FREDERIC JOSEPH PERLAK
PC CL2N15/09,A01H5/00,C07K14/325,CL2N5/10//CL2N1/21,CL2P21/02,PC
(CL2N15/09,CL2R1:07),CL2N15/00,CL2N5/00,CL2N5/00,(CL2N15/00,CL2R1:07) CC
Strandedness: Double;
CC Topology: Linear;
CC Vermin damage-resistant plant
FH Key Location/Qualifiers
FT source 1..661
FT /organism='Unidentified'.
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source
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ORIGIN

Query Match 75.1%; Score 552.4; DB 6; Length 661;
Best Local Similarity 94.4%; Pred. No. 8e-163;
Matches 585; Conservative 0; Mismatches 31; Indels 4; Gaps 1;

Qy 116 TCTGCACTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 175
Db 20 TCGATGTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 79
Qy 176 CAGCTATCTGCTACTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGCCACTACAAATGCC 235
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Qy	236	ATCATTTGGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTGGTCCCAAAG	295
Db	140	ATCATTTGGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTGGTCCCAAAG	199
Qy	296	ATGGACCCCAACCCAGGAGGAGCATCGTGGAAAAGAGAGCGTTCACACACGCTTTCAA	355
Db	200	ATGGACCCCAACCCAGGAGGAGCATCGTGGAAAAGAGAGCGTTCACACACGCTTTCAA	259
Qy	356	AGCAAGTGGATTGATGTGAT----TGCAAGTGAGACTTTTCAACAAAGGGTAATATCGGGA	411
Db	260	AGCAAGTGGATTGATGTGATCGGATCGGATGTCGAGACTTTTCAACAAAGGGTAATATCGGGA	319
Qy	412	AACCTCTCGGATTCCCAATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAG	471
Db	320	AACCTCTCGGATTCCCAATTCGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAAG	379
Qy	472	GAAGTGGCACTACAAATGCCATCTTGGGATTAAGGAAGGCTATCGTTCAAGATGCC	531
Db	380	GAAGTGGCTCCTACAAATGCCATCTTGGGATTAAGGAAGGCTATCGTTGAAGATGCC	439
Qy	532	TCTGCCGACAGTGTCCCAAAGATGGACCCCAACGAGGAGCATCGTGGAAAAAGAA	591
Db	440	TCTGCCGACAGTGTCCCAAAGATGGACCCCAACGAGGAGCATCGTGGAAAAAGAA	499
Qy	592	GACGTTCCAAACCAAGTGTCAAAAGCAAGTGAATGATGTGATATCTCCACTGACGTAAGG	651
Db	500	GACGTTCCAAACCAAGTGTCAAAAGCAAGTGAATGATGTGATATCTCCACTGACGTAAGG	559
Qy	652	GATCAGGCACAAATCCCACTATCCTTCGCAAGACCCCTTCTCTATATAAGGAAGTTCAATTT	711
Db	560	GATCAGGCACAAATCCCACTATCCTTCGCAAGACCCCTTCTCTATATAAGGAAGTTCAATTT	619
Qy	712	CATTGGAGAGCACACGCTG 731	
Db	620	CATTGGAGAGCACACGCTG 639	

Search completed: October 11, 2005, 17:46:12
Job time : 7677 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 14:55:23 ; Search time 1159 Seconds
(without alignments)
3759.215 Million cell updates/sec

Title: US-10-075-105c-1

Perfect score: 736

Sequence: 1 ggatccagcgtgtctctcc.....ggagaggacacgttgatcc 736

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870567 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002as.*
- 7: Geneseq2002bs.*
- 8: Geneseq2003as.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
- 11: Geneseq2003ds.*
- 12: Geneseq2004as.*
- 13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	734.4	99.8	736	ABS53103	Abs53103 Transgene
2	597.4	81.2	1360	ABS53105	Abs53105 Transgene
3	554	75.3	661	AAN81003	Aan81003 Enhanced
4	554	75.3	661	AAN91710	Aan91710 Enhanced
5	554	75.3	2107	AAD01017	Aad01017 Expressio
6	554	75.3	2122	AAD01015	Aad01015 Expressio
7	554	75.3	2436	AAD01018	Aad01018 Expressio
8	554	75.3	3469	AAD51646	Aad51646 Bacillus
9	554	75.3	3469	10 AAD61794	Aad61794 Bt.cry3Bb
10	554	75.3	3469	10 ABX95190	Abx95190 B. thurin
11	554	75.3	3754	3 AAZ51642	Aaz51642 Bacillus
12	554	75.3	3754	10 AAD61790	Aad61790 Bt.cry3Bb
13	554	75.3	3754	10 ABX95186	Abx95186 B. thurin
14	554	75.3	5170	12 ADK98488	Adk98488 B thuring
15	554	75.3	5600	12 ADK98490	Adk98490 B thuring
16	554	75.3	8012	2 AAX57305	Aax57305 Sugar bee
17	554	75.3	8349	3 AAX15565	Aax15565 pMON30464
18	554	75.3	8418	2 AAX57309	Aax57309 Sugar bee
19	554	75.3	8798	2 AAX57308	Aax57308 Sugar bee
20	551.4	74.9	1030	2 AAV53707	AAV53707 Nucleotid

c	21	551.4	74.9	5796	4	AAH25975	Aah25975 Plant exp
	22	551.4	74.9	5897	2	AAV63741	Aav63741 Plasmid p
c	23	551.4	74.9	9361	3	AAD01285	Aad01285 Rice tran
c	24	551.4	74.9	10629	3	AAD01286	Aad01286 Rice tran
	25	550.4	74.8	9335	2	AAV63734	Aav63734 Plasmid p
	26	550	74.7	10249	3	AAAI5563	Aaai5563 pMON33828
	27	550	74.7	10312	3	AAAI5564	Aaai5564 pMON33829
	28	550	74.7	10339	3	AAAI5562	Aaai5562 pMON33827
	29	549.8	74.7	1030	2	AAQ68893	Aaq68893 Promoter
	30	548.4	74.5	1030	2	AAQ76263	Aaq76263 PNA lecti
	31	548.4	74.5	10160	2	AAV63723	Aav63723 Vector pl
	32	548.4	74.5	11784	2	AAV63724	Aav63724 Vector pl
	33	548.4	74.5	11991	2	AAV63725	Aav63725 Vector pl
	34	543.6	73.9	4149	3	AAZ51641	Aaz51641 Bacillus
	35	543.6	73.9	4149	10	AAD61789	Aad61789 Bt.cry3Bb
	36	543.6	73.9	4149	10	ABX95185	Abx95185 B. thurin
	37	534.6	72.6	5767	6	AAI17547	Aai17547 Plasmid p
	38	534.6	72.6	14446	6	AAI17548	Aai17548 Plasmid p
	39	526	71.5	829	4	AAF81265	Aaf81265 Cauliflow
	40	526	71.5	829	9	ADA44822	Ada44822 Cauliflow
	41	526	71.5	1334	2	AAZ27627	Aaz27627 Plasmid S
c	42	526	71.5	11478	8	ABV75873	Abv75873 Vector pp
	43	526	71.5	12304	8	ABV75876	Abv75876 Luciferas
c	44	526	71.5	12497	8	ABV75875	Abv75875 Luciferas
	45	526	71.5	12614	4	AAC66931	Aac66931 Plant sig

ALIGNMENTS

RESULT 1
ABS53103
ID ABS53103 standard; DNA; 736 BP.
XX
AC ABS53103;
XX
DT 29-NOV-2002 (first entry)
XX
DE Transgene expression related bidirectional dual promoter complex #1.
KW Bidirectional dual promoter complex; transcription; transgene;
KW agronomic performance; transformation; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..736
FT /tag= a
FT /note= "The complement of this sequence is also claimed
in claim 9 as SEQ ID number 2"
XX
FN WO200264804-A2.
XX
PD 22-AUG-2002.
XX
PF 13-FEB-2002; 2002WO-US004188.
XX
PR 13-FEB-2001; 2001US-0268358P.
XX
PA (UYFL) UNIV FLORIDA.
XX
PI Li Z, Gray DJ;
XX
DR WPI; 2002-627601/67.
XX
PT New bi-directional promoter complex comprising a modified enhancer region
including at least 2 enhancer sequences, and at least 2 core promoters,
useful for enhancing or improving transcriptional activity of transgenes.
XX
PS Claim 9; Fig 2; 77pp; English.
XX
CC The invention describes a bi-directional promoter complex comprising a
modified enhancer region that includes at least 2 enhancer sequences, and

CC at least 2 core promoters. The core promoters are on either side of the
CC modified enhancer region in a divergent orientation. The bi-directional
CC promoter complex is useful for enhancing transcriptional activity of
CC transgenes to improve agronomic performance used in genetic
CC transformation with plants. Vectors that include the bi-directional
CC promoter complex may be used to express foreign genes in mammalian cells
CC and in plant cells including dicots and monocots. This sequence
CC represents a bidirectional dual promoter complex useful for enhancing
CC transcriptional activity of transgenes
XX

SQ Sequence 736 BP; 222 A; 176 C; 175 G; 163 T; 0 U; 0 Other;

Query Match 99.8%; Score 734.4; DB 6; Length 736;

Best Local Similarity 99.9%; Pred. No. 6.9e-232;

Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGATCAGCGTGCCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCTTGGC 60

DB 1 GGATCAGCGTGCCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCTTGGC 60

QY 61 AAGGATAGTGGATTGTGCGTCACTCCCTTACGTCAGTGGAGATCTGCAGAAGCTTCTGC 120

DB 61 AAGGATAGTGGATTGTGCGTCACTCCCTTACGTCAGTGGAGATCTGCAGAAGCTTCTGC 120

QY 121 AGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTCGGATTCCATTGCCAGCT 180

DB 121 AGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTCGGATTCCATTGCCAGCT 180

QY 181 ATCTGTCACTTCATCAAAAGGACAGTAGAAGAGGGTGGCACCTTACAAATGCCATCAT 240

DB 181 ATCTGTCACTTCATCAAAAGGACAGTAGAAGAGGGTGGCACCTTACAAATGCCATCAT 240

QY 241 TGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCACAGTGGTCCCAAGATGGA 300

DB 241 TGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCACAGTGGTCCCAAGATGGA 300

QY 301 CCCCCACCCAGGAGCATCGTGGAAAAAGAGACGTTTCCAAACACGCTTCCAAAGCAA 360

DB 301 CCCCCACCCAGGAGCATCGTGGAAAAAGAGACGTTTCCAAACACGCTTCCAAAGCAA 360

QY 361 GTGGATTGATGTATTCAGTGGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTC 420

DB 361 GTGGATTGATGTATTCAGTGGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTC 420

QY 421 GGATTCATTGCCAGCTATCTGTCACTTCCATCAAAAGGACAGTAGAAGAGGGTGGC 480

DB 421 GGATTCATTGCCAGCTATCTGTCACTTCCATCAAAAGGACAGTAGAAGAGGGTGGC 480

QY 481 ACCTACAAATGCCATATTCGATAAGAGGAGCTATCGTTCAAGATGCTCTGCGGAC 540

DB 481 ACCTACAAATGCCATATTCGATAAGAGGAGCTATCGTTCAAGATGCTCTGCGGAC 540

QY 541 AGTGTGCCAAAGATGAGACCCCAACAGAGAGCATCGTGAAAAAGAGAGCTTCCA 600

DB 541 AGTGTGCCAAAGATGAGACCCCAACAGAGAGCATCGTGAAAAAGAGAGCTTCCA 600

QY 601 ACCAGCTCTTCAAGCAAGTGGATTGATGTATCTCCACTGACGTAAGGGATGAGCA 660

DB 601 ACCAGCTCTTCAAGCAAGTGGATTGATGTATCTCCACTGACGTAAGGGATGAGCA 660

QY 661 CAATCCCACTATCTTCCGAGACCCCTTCTCTATATAGGAAGTTCATTTGGAG 720

DB 661 CAATCCCACTATCTTCCGAGACCCCTTCTCTATATAGGAAGTTCATTTGGAG 720

QY 721 AGACAGCTGGATCC 736

DB 721 AGACAGCTGGATCC 736

RESULT 2

ABS53105

ID ABS53105 standard; DNA; 1360 BP.

XX

AC ABS53105;
XX 29-NOV-2002 (first entry)
XX Transgene expression related bidirectional dual promoter complex #2.
XX Bidirectional dual promoter complex; transgene;
XX agronomic performance; transformation; ds.
XX Synthetic.
XX

Key Location/Qualifiers

FT misc_feature 1..1360

FT /tag= a

FT /note= "The complement of this sequence is also claimed

FT in claim 10 as SEQ ID number 4"

XX WO200264804-A2.

XX 22-AUG-2002.

XX 13-FEB-2002; 2002WO-US004188.

XX 13-FEB-2001; 2001US-0268358P.

XX (UYFL) UNIV FLORIDA.

XX Li Z, Gray DJ;

XX WPI; 2002-627601/67.

XX New bi-directional promoter complex comprising a modified enhancer region
XX including at least 2 enhancer sequences, and at least 2 core promoters,
XX useful for enhancing or improving transcriptional activity of transgenes.
PS Claim 10; Fig 4; 77pp; English.

XX The invention describes a bi-directional promoter complex comprising a
XX modified enhancer region that includes at least 2 enhancer sequences, and
XX at least 2 core promoters. The core promoters are on either side of the
XX modified enhancer region in a divergent orientation. The bi-directional
XX promoter complex is useful for enhancing transcriptional activity of
XX transgenes to improve agronomic performance used in genetic
XX transformation with plants. Vectors that include the bi-directional
XX promoter complex may be used to express foreign genes in mammalian cells
XX and in plant cells including dicots and monocots. This sequence
XX represents a bidirectional dual promoter complex useful for enhancing
XX transcriptional activity of transgenes

SQ Sequence 1360 BP; 353 A; 319 C; 317 G; 371 T; 0 U; 0 Other;

Query Match 81.2%; Score 597.4; DB 6; Length 1360;

Best Local Similarity 99.8%; Pred. No. 1.1e-186;

Matches 598; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 109 AGAAGCTTCTGCAGTGCAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTCGGATTC 168

DB 762 ATAAAGCTTCTGCAGTGCAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTCGGATTC 821

QY 169 CATTTGCCAGCTATCTGTCACTTCAATCAAAAGGACAGTAGAAGAGGGTGGCAGCTAC 228

DB 822 CATTTGCCAGCTATCTGTCACTTCAATCAAAAGGACAGTAGAAGAGGGTGGCAGCTAC 881

QY 229 AATGCGCATCATTCGATAAAGGAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGT 288

DB 882 AATGCGCATCATTCGATAAAGGAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGT 941

QY 289 CCAAGAGATGGACCCCAACAGGAGCATCGTGAAAAAGAGAGCTTCCAACCCACG 348

DB 942 CCAAGAGATGGACCCCAACAGGAGCATCGTGAAAAAGAGAGCTTCCAACCCACG 1001

QY 349 TCTTCAAGCAAGTGGATTCATGTGATTCAGTGAGACTTTTCAACAAAGGGTAATATCG 408

XX

Db 1002 TCCTCAAGCAAGTGGATTGATGTGATGCGAGTCTTTCAACAAGGTTAATATCG 1061
 Qy 409 GGAACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAA 468
 Db 1062 GGAACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAA 1121.
 Qy 469 AAGGAAGTGGCAGCTACAAATGCATTCATTCGCATTAAGAAAGGCTATCGTTCAAGAT 528
 Db 1122 AAGGAAGTGGCAGCTACAAATGCATTCATTCGCATTAAGAAAGGCTATCGTTCAAGAT 1181
 Qy 529 GCCTCTGCCGACAGTGGTCCCAAGATGGACCCACCACGAGGAGCATCGTGGAAAAA 588
 Db 1182 GCCTCTGCCGACAGTGGTCCCAAGATGGACCCACCACGAGGAGCATCGTGGAAAAA 1241
 Qy 589 GAAGACGTTCCAAACCCAGTCTTCAAGCAAGTGGATGTGATATCTCCACTGACGTA 648
 Db 1242 GAAGACGTTCCAAACCCAGTCTTCAAGCAAGTGGATGTGATATCTCCACTGACGTA 1301
 Qy 649 AGGATGACGCACAAATCCCACTATCTTCCGAAGCCCTTCTCTATATAAGGAAGTTC 707
 Db 1302 AGGATGACGCACAAATCCCACTATCTTCCGAAGCCCTTCTCTATATAAGGAAGTTC 1360

RESULT 3

AAN81003
 ID AAN81003 standard; DNA; 661 BP.
 XX AC AAN81003;

XX 03-NOV-1990 (first entry)

DE Enhanced CamV35S promoter used in pMON893 B.thuringiensis toxin prodn.

XX Bacillus thuringiensis var. tenebrionis toxin gene; enhanced promoter;
 KW CamV35S; pMON893; Coleopteran insects; transformed plants;
 KW chimaeric gene; ss.

XX Bacillus thuringiensis.

XX Key Location/Qualifiers
 FT misc_feature 27..279
 FT /*tag= a
 FT /number= 1
 FT /note= "duplicated enhancer"
 FT 289..541
 FT /*tag= b
 FT /number= 2
 FT /note= "duplicated enhancer"

XX EP289479-A.

PN 02-NOV-1988.

XX 26-APR-1988; 88EP-00870070.

XX 29-APR-1987; 87US-00044081.

XX (MONS) MONSANTO CO.

XX Fischhoff DA, Fuchs RL, Mcpherson SA, Lavrik PB, Perlak FJ;

XX WPI; 1988-309416/44.

XX Genetically transformed plants with toxicity to Coleopteran insects -
 PT obtd. using chimeric gene contg. sequence encoding toxin protein of
 PT Bacillus thuringiensis.

XX Disclosure; Page ?; 52pp; English.

XX A fragment of the CamV35S promoter (-343 to +9), previously constructed
 CC by Odell et al. (1985) Nature 313:810-812, is necessary for maximal
 CC expression of the promoter. It was excised as a ClaI-HindIII fragment,
 CC made blunt ended with DNA pol I and inserted into the HindII site of

CC pUC18. The upstream region of the 35S promoter was excised from this
 CC plasmid as a HindIII-EcoRV fragment (-343 to -90) and inserted into the
 CC same plasmid between the HindIII and PstI sites. The enhanced promoter
 CC thus contains a duplication of sequences -343 to -90. See also AAN81000-
 XX N81003

SQ Sequence 661 BP; 194 A; 160 C; 157 G; 150 T; 0 U; 0 Other;

Query Match 75.3%; Score 554; DB 1; Length 661;

Best Local Similarity 94.5%; Pred. No. 2.9e-172;

Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGCGTGAAGCTTTTCAACAAGGTTAATATCGGAAACCTCTCGGATTCATTGCC 175

Db 20 TCCGATGTGAGACTTTTCAACAAGGTTAATATCGGAAACCTCTCGGATTCATTGCC 79

Qy 176 CAGCTATCTGCTCACTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCACCTACAAATGCC 235

Db 80 CAGCTATCTGCTCACTTTTGTGAAGATAGTGGAAAAGGAGGTGGCTCTTACAAATGCC 139

Qy 236 ATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295

Db 140 ATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 199

Qy 296 ATGGAACCCACCCACGAGGAGCATCGTGGAAAAGGAGGTGGCACCTACAAATGCC 355

Db 200 ATGGAACCCACCCACGAGGAGCATCGTGGAAAAGGAGGTGGCACCTACAAATGCC 259

Qy 356 AGCAAGTGGATTGATGTGAT---TGCAGTGAGACTTTTCAACAAGGTTAATATCGGA 411

Db 260 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAGGTTAATATCGGA 319

Qy 412 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCACTCAAAAGGACAGTAGAAAAG 471

Db 320 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTATTTGTGAAGATAGTGGAAAAG 379

Qy 472 GAAGTGGGACCTACAAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC 531

Db 380 GAAGTGGGCTCTTACAAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTGAAGATGCC 439

Qy 532 TCTGCCGACAGTGTCTCCAAAGATGGACCCACCCACGAGGAGCATCGTGGAAAAGAA 591

Db 440 TCTGCCGACAGTGTCTCCAAAGATGGACCCACCCACGAGGAGCATCGTGGAAAAGAA 499

Qy 592 GAGCTTCCAAACCCAGCTTTTCAAAAGCAAGTGGATTTGATATCTCCACTGACGTAAGG 651

Db 500 GAGCTTCCAAACCCAGCTTTTCAAAAGCAAGTGGATTTGATATCTCCACTGACGTAAGG 559

Qy 652 GATGACGACAAATCCCACTATCTTCCGAAGACCTTCTCTATATAAGGAAGTTCATTT 711

Db 560 GATGACGACAAATCCCACTATCTTCCGAAGACCTTCTCTATATAAGGAAGTTCATTT 619

Qy 712 CATTTGGAGAGGACACGCTG 731

Db 620 CATTTGGAGAGGACACGCTG 639

RESULT 4

AAN91710

ID AAN91710 standard; DNA; 661 BP.

XX AC AAN91710;

XX 25-MAR-2003 (revised)

DT 12-MAR-1990 (first entry)

XX Enhanced CamV35S promoter used in plasmid pMON893.

XX CamV35S promoter; Bacillus thuringiensis; toxin protein; insecticide;
 KW plasmid pMON893.

XX Cauliflower mosaic virus.


```
CC herbicides such as glyphosate and AMPA tolerance, in recombinant plants
CC and to prevent self-fertilisation and enhance hetero-fertilisation. The
CC present DNA sequence is the expression cassette-2, comprising a plant
CC operable promoter and 5' sequences like, 5' untranslated region (UTR) and
CC intron, linked to modified E. coli phnO coding region encoding P2A AMPA
CC acyltransferase (AAT) enzyme and plant operable termination sequences
XX
SQ Sequence 2122 BP; 495 A; 537 C; 561 G; 529 T; 0 U; 0 Other;

Query Match 75.3%; Score 554; DB 3; Length 2122;
Best Local Similarity 94.5%; Pred. No. 5.1e-172;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCGAGTGAGACTTTTCAACAAGGCTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 8 TCCGATGTGAGACTTTTCAACAAGGCTAATATCGGAAACCTCTCGGATTCATTGCC 67

Qy 176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAGAGTGCGACCTACAAATGCC 235
Db 68 CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAGTGCTCTACAAATGCC 127

Qy 236 ATCATTCGGATAAAGGAAAGCTATCGTTCAAGATGCTCTGCGACAGTGGTCCAAAG 295
Db 128 ATCATTCGGATAAAGGAAAGGCCATCGTTGAAGATGCTCTGCGACAGTGGTCCAAAG 187

Qy 296 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGAGACGTTTCCACACCGTCTTCAA 355
Db 188 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGAGACGTTTCCACACCGTCTTCAA 247

Qy 356 AGCAAGTGGATTGATGTGAT-----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGA 411
Db 248 AGCAAGTGGATTGATGTGATGTGTCGATGTGAGACTTTTCAACAAAGGGTAATATCGGA 307

Qy 412 AACCTCTCGGATTCGATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
Db 308 AACCTCTCGGATTCGATTCGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 367

Qy 472 GAAGGTGGCACTACAATGCGCATCTTGGGATAAAGGAAGGCTATCGTTCAAGATGCC 531
Db 368 GAAGTGGCTCTACAATGCGCATCTTGGGATAAAGGAAGGCTATCGTTGAAGATGCC 427

Qy 532 TCTGCCACAGTGTGCCAAGATGGACCCGCCACGAGGAGCATCGTGGAAAAAGAA 591
Db 428 TCTGCCACAGTGTGCCAAGATGGACCCGCCACGAGGAGCATCGTGGAAAAAGAA 487

Qy 592 GACGTTTCCACCACTCTTCAACCAAGTGGATTGATGTGATATCTCCACTGACGTAAG 651
Db 488 GACGTTTCCACCACTCTTCAACCAAGTGGATTGATGTGATATCTCCACTGACGTAAG 547

Qy 652 GATCAGCGACAATCCCACTATCCTTCGCAAGACCTTCTCTATATAAGGAAGTTCATTT 711
Db 548 GATCAGCGACANATCCCACTATCCTTCGCAAGACCTTCTCTATATAAGGAAGTTCATTT 607

Qy 712 CATTGGAGAGGACACGCTG 731
Db 608 CATTGGAGAGGACACGCTG 627

RESULT 7
AAD01018
ID AAD01018 standard; DNA; 2436 BP.
XX
AC AAD01018;
XX
XX
DT 21-SEP-2000 (first entry)
XX
DE Expression cassette-5 comprising modified E. coli P2A phnO coding gene.
XX
KW Phosphonate herbicide tolerance; aminomethyl phosphonic acid; AMPA; AAT;
KW acyltransferase; transacylase; recombinant plant; expression cassette;
KW corn; tobacco; wheat; cotton; canola; rice; chloroplast transit peptide;
KW CTP; glyophosate oxidase; GOX; glyophosate oxidoreductase; phnO gene;
KW self-fertilisation; hetero-fertilisation; ds.
```

```
XX Escherichia coli.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT promoter 26..640
FT intron 670..1473
FT /tag= a
FT /note= "Plant functional heterologous promoter"
FT /tag= b
FT /note= "Enhances expression of the phnO gene"
FT transit_peptide 1498..1725
FT /tag= c
FT /note= "Targets the protein to an intracellular
FT organelle, like chloroplast"
FT 1726..2160
FT CDS
FT /tag= d
FT /product= "Escherichia coli modified P2A AMPA
FT acyltransferase (AAT) enzyme"
FT /function= "Transfers acyl group from an acylcarrier
FT (CoA) to the free amino group of aminomethylphosphonate"
FT 2172..2427
FT terminator
FT /tag= e
XX WO200029596-A1.
PN
XX 25-MAY-2000.
PD
XX
PF 16-NOV-1999; 99WO-US027152.
PR 17-NOV-1998; 98US-0108763P.
XX (MONS ) MONSANTO CO.
XX
XX Barry GF;
PI
XX WPI; 2000-387806/33.
DR P-PSDB; AAY71251.
XX
XX Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat,
PT cotton, canola and rice plants involves transforming plants with
PT phosphonate metabolizing genes encoding acyltransferase enzyme.
XX
XX Disclosure; Page 173-175; 179pp; English.
XX
XX The patent discloses a method for selectively enhancing the phosphonate
CC herbicide tolerance in recombinant corn, tobacco, wheat, cotton, canola
CC and rice plants, by transforming the plants with an expression cassette.
CC It comprises of a structural DNA sequence, that encodes an aminomethyl
CC phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of
CC N-acylation of AMPA. This sequence has an amino terminal chloroplast
CC transit peptide (CTP), that targets AAT to the chloroplast. Co-expression
CC of glyphosate oxidase (GOX) gene, encoding glyphosate oxidoreductase,
CC along with AAT provides the transformed plants with higher resistance to
CC phosphonate herbicides. This method is useful for enhancing phosphonate
CC herbicides such as glyphosate and AMPA tolerance, in recombinant plants
CC and to prevent self-fertilisation and enhance hetero-fertilisation. The
CC present DNA sequence is the expression cassette-5, comprising a plant
CC operable promoter and 5' sequences like intron, linked to modified E.
CC coli phnO coding region, encoding P2A AMPA acyltransferase (AAT) enzyme
CC and plant operable termination sequences
XX
SQ Sequence 2436 BP; 634 A; 565 C; 567 G; 670 T; 0 U; 0 Other;

Query Match 75.3%; Score 554; DB 3; Length 2436;
Best Local Similarity 94.5%; Pred. No. 5.5e-172;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCGAGTGAGACTTTTCAACAAGGCTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAGGCTAATATCGGAAACCTCTCGGATTCATTGCC 87

Qy 176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGCACCTACAAATGCC 235
```



```
Db 88 CAGCTATCTGTCACCTTTATTTGTAAGATAGTGGAAAGGAGGTTGGCTCTACAAATGCC 147
Qy 236 ATCATTTGGATAAAGGAAAGGCTATCGTTTCAAGATGCTCTGCCACACAGTGGTCCCAAAG 295
Db 148 ATCATTTGGATAAAGGAAAGGCTATCGTTTCAAGATGCTCTGCCACACAGTGGTCCCAAAG 207
Qy 296 ATGAGCCCCCACCACAGAGAGCATCGTGGGAAAAAGAAAGAGAGTTCACACACGCTTCAA 355
Db 208 ATGAGCCCCCACCACAGAGAGCATCGTGGGAAAAAGAAAGAGAGTTCACACACGCTTCAA 267
Qy 356 AGCAAGTGGATTGATGTCAT---TGCAGTGCAGACTTTTCAACAAAGGTAATATCCGGA 411
Db 268 AGCAAGTGGATTGATGTCATGTCGATGTCGATGTCGAGACTTTTCAACAAAGGTAATATCCGGA 327
Qy 412 AACCTCTCTCGGATTCATTTGCCAGCTATCTGTCTACATTTTCATCAAAAGGACAGTAGAAAAAG 471
Db 328 AACCTCTCTCGGATTCATTTGCCAGCTATCTGTCTACATTTTCATCAAAAGGACAGTAGAAAAAG 387
Qy 472 GAAGTGGCAGCTACAAATGCCATCATTTGGCAGTATCGGATAAAGGAGGCTATCGTTCAAAGTCC 531
Db 388 GAAGTGGCAGCTACAAATGCCATCATTTGGCAGTATCGGATAAAGGAGGCTATCGTTCAAAGTCC 447
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCACCACCCAGGAGCATCGTGGAAAAAGAA 591
Db 448 TCTGCCGACAGTGGTCCCAAGATGGACCCACCACCCAGGAGCATCGTGGAAAAAGAA 507
Qy 592 GACGTTCCCAACACAGCTCTTCAAGCAAGTGAATGATGATATCTCCACTGACGTAAGG 651
Db 508 GACGTTCCCAACACAGCTCTTCAAGCAAGTGAATGATGATATCTCCACTGACGTAAGG 567
Qy 652 GATGAGCAGCAATCCCACTATCTCTTCCAGAACCCCTTCTCTATATAAGGAAGTTCAATT 711
Db 568 GATGAGCAGCAATCCCACTATCTCTTCCAGAACCCCTTCTCTATATAAGGAAGTTCAATT 627
Qy 712 CATTGGAGAGGACACGCTG 731
Db 628 CATTGGAGAGGACACGCTG 647
```

RESULT 8

AAZ51646

ID AAZ51646 standard; DNA; 3469 BP.

XX AC AAZ51646;

XX AC

DT 15-SEP-2003 (revised)

DT 21-JUN-2000 (first entry)

XX

DE Bacillus thuringiensis Cry3Bb variant 11231mv2 expression cassette-2.

XX delta-endotoxin; Cry3B; Bt toxin; crystal protein; insect pest;

KW insecticide; Coleopteran; expression cassette; transgenic plant;

KW Cry3Bb variant 11231mv2, ds.

KW

OS Cauliflower mosaic virus.

OS Triticum aestivum.

OS Oryza sativa.

OS Bacillus thuringiensis.

OS Chimeric.

XX

Key Location/Qualifiers

FT promoter 25..640

FT /*tag= a

FT /label= P-CaWV.35S

FT 5'UTR 664..734

FT /*tag= b

FT /label= L-Ta.hcb1

FT /note= "Wheat chlorophyll A/B binding protein

FT untranslated leader sequence"

FT intron 748..1238

FT /*tag= c

FT /label= I-Os.Act1

FT

FT CDS /note= "Rice actin intron sequence"

FT 1241..3202

FT /*tag= d

FT /product= "Cry3Bb variant 11231mv2"

FT terminator 3217..3450

FT /*tag= e

FT /label= T-Ta.hspl17

FT /note= "Wheat heat shock Hspl17 transcription termination

FT and polyadenylation sequence"

XX

PN WO200011185-A2.

XX

PD 02-MAR-2000.

XX

PF 19-AUG-1999; 99WO-US018883.

XX

PR 19-AUG-1998; 98US-0097150P.

XX

XX (MONS) MONSANTO CO.

PA Romano CP;

XX

PI WPI: 2000-246568/21.

XX

XX P-PSDB; AAY70446.

DR

XX Novel expression cassettes which express Bacillus thuringiensis Cry3

PT delta-endotoxin portion which is toxic to coleopteran insect pests,

PT useful for producing transgenic plants with improved insecticidal

PT activity.

XX

PS Claim 16; Page 149-152; 17lpp; English.

XX

CC The present sequence is an expression cassette from a Cry3Bb plant

CC expression vector pMON33748. It comprises an enhanced Cauliflower mosaic

CC virus (CaMV) 35S promoter sequence, a wheat chlorophyll A/B binding

CC protein untranslated leader sequence, a rice actin intron sequence, a

CC Bacillus thuringiensis delta-endotoxin Cry3Bb variant 11231mv2 coding

CC sequence and a wheat heat shock Hspl17 transcription termination and

CC polyadenylation sequence. This expression cassette is used to improve

CC expression of Cry3B variant protein in transgenic plants e.g. maize, to

CC increase insecticidal activity against Coleopteran pests. (Updated on 15-

CC SEP-2003 to standardise OS field)

XX

SQ Sequence 3469 BP; 790 A; 1078 C; 845 G; 756 T; 0 U; 0 Other;

Query Match 75.3%; Score 554; DB 3; Length 3469;

Best Local Similarity 94.5%; Pred. No. 6.5e-172;

Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGAGTGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCTCGGATTCATTGCC 175

Db 28 TCCGATGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCTCGGATTCATTGCC 87

Qy 176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAGGAGGTCGACCTACAAATGCC 235

Db 88 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAGGAGGTCGACCTACAAATGCC 147

Qy 236 ATCAATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTCGGACAGTGGTCCCAAAG 295

Db 148 ATCAATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTCGGACAGTGGTCCCAAAG 207

Qy 296 ATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAAAGACGTTTCCAAACACGCTTCAA 355

Db 208 ATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAAAGACGTTTCCAAACACGCTTCAA 267

Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCCGGA 411

Db 268 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 327

Qy 412 AACCTCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCAATCAAAAGGACAGTAGAAAAAG 471

Db 328 AACCTCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCAATCAAAAGGACAGTAGAAAAAG 387

Qy	472	GAAGGTGCACCTCAAAATGCCATCATTTGCGGATAAAGAAAGGCTATCGTTCAAGATGCC	533
Db	388	GAAGGTGGCTCCTCAAAATGCCATCATTTGCGGATAAAGAAAGGCTATCGTTCAAGATGCC	447
Qy	532	TCTGCCGACAGTGGTCCCAAAGATGCAGCCCCCACCACGAGGAGCATCGTGAAAAAGAA	591
Db	448	TCTGCCGACAGTGGTCCCAAAGATGCAGCCCCCACCACGAGGAGCATCGTGAAAAAGAA	507
Qy	592	GACGTTCCAAACACAGCTTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG	651
Db	508	GACGTTCCAAACACAGCTTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG	567
Qy	652	GATGACGCACAATCCCACTATCTCTTCGCAAGACCCCTTCTCTATATAGGAAGTTCATTT	711
Db	568	GATGACGCACAATCCCACTATCTCTTCGCAAGACCCCTTCTCTATATAGGAAGTTCATTT	627
Qy	712	CATTTGGAGAGACACGCTG 731	
Db	628	CATTTGGAGAGACACGCTG 647	
RESULT 9			
AAD61794			
XX	ID	AAD61794 standard; DNA; 3469 BP.	
XX	AC	AAD61794;	
XX	AC	AAD61794;	
XX	DT	15-JAN-2004 (first entry)	
XX	DE	Bt.cry3Bb.1l23lmv2 expression vector DNA, pMON33748.	
XX	KW	Transgenic plant; Cry3Bb-delta-endotoxin; Coleopteran pest resistance;	
XX	KW	insecticide; variant; cyclic; circular; chimeric; rice; wheat; gene; ds.	
XX	OS	Chimeric - Cauliflower mosaic virus.	
XX	OS	Chimeric - Oryza sativa.	
XX	OS	Chimeric - Bacillus thuringiensis.	
XX	OS	Chimeric - Triticum aestivum.	
XX	XX		
FH	Key	Location/Qualifiers	
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FT		/*tag= a	
FT		/note= "Cauliflower mosaic virus 35S promoter (P-	
FT		CaMV.35S)"	
FT	misc_feature	664..734	
FT		/*tag= b	
FT		/note= "Wheat chlorophyll A/B binding protein	
FT		untranslated leader sequence (L-Ta.hcb1)"	
FT	intron	748..1238	
FT		/*tag= c	
FT		/note= "Rice actin intron (I-Os.Act1)"	
FT	CDS	1241..3202	
FT		/*tag= d	
FT		/product= "Bt.cry3Bb.1l23lmv2 protein"	
FT	misc_feature	3217..3420	
FT		/*tag= e	
FT		/note= "Wheat heat shock Hspl17 transcription termination	
FT		and polyadenylation sequence (T-Ta.Hspl17)"	
XX			
PN	US2003115630-A1.		
XX			
XX	19-JUN-2003.		
XX			
PF	29-AUG-2002; 2002US-00232665.		
XX			
PR	19-AUG-1999; 99US-00377466.		
XX			
PA	(ROMA/) ROMANO C P.		
XX			
PI	Romano CP;		
XX			
XX	WPI; 2003-810928/76.		
DR	P-PSDB; ABW01055.		

XX	New transgenic plant resistant to Coleopteran pests, comprises Bacillus thuringiensis Cry3-delta-endotoxin gene.									
PT	Claim 16; Page 77-80; Opp; English.									
XX	The invention relates to novel transgenic plants comprising Bacillus thuringiensis Cry3-delta-endotoxin gene or its variants having coleopteran inhibitory activity. The invention is useful for controlling Coleopteran insect infestation in a field of crop plants. The present sequence is B. thuringiensis Cry3Bb-delta-endotoxin variant expression vector DNA									
XX	Sequence	3469 BP; 790 A; 1078 C; 845 G; 756 T; 0 U; 0 Other;								
XX	Query Match	75.3%;	Score	554;	DB	10;	Length	3469;		
XX	Best Local Similarity	94.5%;	Pred.	No.	6.5e-172;					
XX	Matches	586;	Conservative	0;	Mismatches	30;	Indels	4;	Gaps	1;
Qy	116	TCGTCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTCGGATTCATTCGCC	175							
Db	28	TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTCTCGGATTCATTCGCC	87							
Qy	176	CAGCTATCTGTCTACTTTCATCAAAAGACAGTAGAAAGGAAGTGGCACCCTACAAATGCC	235							
Db	88	CAGCTATCTGTCTACTTTCATCAAAAGACAGTAGTGGAAAGGAAGTGGCTCTCTACAAATGCC	147							
Qy	236	ATCATTTGCGATAAAGGAAGGGCTATCGTTCAAGATCGCTCTGCGGACAGTGGTCCCAAAG	295							
Db	148	ATCATTTGCGATAAAGGAAGGGCCATCGTTGAAGATGCTCTGCGGACAGTGGTCCCAAAG	207							
Qy	296	ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGGAAGAGCGTTCCAAACACGCTTTCAA	355							
Db	208	ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGGAAGAGCGTTCCAAACACGCTTTCAA	267							
Qy	356	AGCAAGTGGATTGATGTGAT----TCGAGTGAGACTTTTCAACAAAGGGTAAATATCGGA	411							
Db	268	AGCAAGTGGATTGATGTGATGTTGGTCCGATGTGAGACTTTTCAACAAAGGGTAAATATCGGA	327							
Qy	412	AACCTCTCGGATTCCATTGCCAGCGTATCTGTCACCTTCATCAAAAGGACAGTAGAAAAG	471							
Db	328	AACCTCTCGGATTCCATTGCCAGCGTATCTGTCACCTTTATTTGTAAGATAGTGGAAAAG	387							
Qy	472	GAAGGTGGCACCTACAAATGCCATCATTCGCGATAAAGGAAGGCTATCGTTCAAGATGCC	531							
Db	388	GAAGGTGGCTCTACAAATGCCATCATTCGATAAAGGAAGGCCATCGTTGAAGATGCC	447							
Qy	532	TCTGCGGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCTGTGGAAAAGAA	591							
Db	448	TCTGCGGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCTGTGGAAAAGAA	507							
Qy	592	GAGCTTCCACACGCTCTTCAAGCAAGTGGATTGATATCTCCACTGACGCTAAGG	651							
Db	508	GAGCTTCCACACGCTCTTCAAGCAAGTGGATTGATATCTCCACTGACGCTAAGG	567							
Qy	652	GATGACGCAAAATCCCACTATCCCTTCGCAAGACCCCTTCCTCTATATAAGGAAGTTCATTT	711							
Db	568	GATGACGCAAAATCCCACTATCCCTTCGCAAGACCCCTTCCTCTATATAAGGAAGTTCATTT	627							
Qy	712	CATTGAGGAGGACAGCGTG	731							
Db	628	CATTGAGGAGGACAGCGTG	647							
XX	RESULT 10									
XX	ABX95190									
XX	ID	ABX95190 standard; DNA; 3469 BP.								
XX	AC	ABX95190;								
XX	DT	12-JUN-2003 (first entry)								
XX	DE	B. thuringiensis delta endotoxin Cry3Bb1 11231mv2 expression cassette #2.								

CC delta-endotoxin relative to the highest levels obtained using prior
CC compositions. In particular, transgenic maize expressing higher levels of
CC the Cry3Bb protein designed to exhibit increased toxicity toward
CC Coleopteran pests deliver superior levels of insect protection and are
CC less likely to sponsor development of populations of target insects that
CC are resistant to the insecticidally active protein. Improved control of
CC susceptible target insect pests and season long protection from insect
CC pathogens is achieved using the modified polynucleotide. The modified
CC polynucleotide reduces the number of transgenic events that have to be
CC screened in order to identify one which contains beneficial levels of one
CC or more insect controlling compositions. The present sequence represents
CC *Bacillus thuringiensis* delta endotoxin Cry3Bbvl1231 expression cassette
CC #2 DNA
XX
SQ

Sequence 3754 BP; 1030 A; 889 C; 800 G; 1035 T; 0 U; 0 Other;
Query Match 75.3%; Score 554; DB 10; Length 3754;
Best Local Similarity 94.5%; Pred. No. 6.7e-172;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

QY 116 TCTGACGTGACCTTTTCACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 87
QY 176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAGGAGTGGCACCTACAAATGCC 235
Db 88 CAGCTATCTGTCACTTATTGTGAGATAGTGGNAAAGGAGTGGCTCTCTACAAATGCC 147
QY 236 ATCATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGGTCCCAAAG 295
Db 148 ATCATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGGTCCCAAAG 207
QY 296 ATGGACCCCAACCCACGAGGAGCATCTGGAAGAAAGAGCTTCCAAACAGCTCTTCAA 355
Db 208 ATGGACCCCAACCCACGAGGAGCATCTGGAAGAAAGAGCTTCCAAACAGCTCTTCAA 267
QY 356 AGCAAGTGGATTGATGTGAT-----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 268 AGCAAGTGGATTGATGTGATGTGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 327
QY 412 AACCTCTCGGATTCATTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAG 471
Db 328 AACCTCTCGGATTCATTGCCAGCTATCTGTCACTTATTGTGAAGATAGTGGAAAAAG 387
QY 472 GAAGTGGCCACTCAATGCCATCATTCGATTAAGAAAGGCTATCGTTCAGATGCC 531
Db 388 GAAGTGGCTCTCAATGCCATCATTCGATTAAGAAAGGCTATCGTTCAGATGCC 447
QY 532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACGAGGAGCATCGTGGAAAAAGAA 591
Db 448 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACGAGGAGCATCGTGGAAAAAGAA 507
QY 592 GACGTTCCAAACCGCTTTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 651
Db 508 GACGTTCCAAACCGCTTTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 567
QY 652 GATGACCGCAATCCCACTATCTTCCGAAGCCCTCTCTATATAGGAAGTTCATTT 711
Db 568 GATGACCGCAATCCCACTATCTTCCGAAGCCCTCTCTATATAGGAAGTTCATTT 627
QY 712 CATTTGGAGAGGACACGCTG 731
Db 628 CATTTGGAGAGGACACGCTG 647

RESULT 14
ADK98488
ID ADK98488 standard; DNA; 5170 BP.
XX
AC ADK98488;
XX
XX 03-JUN-2004 (first entry)
DT
XX

DE B thuringiensis cry1Bb-related expression cassette DNA SeqID11.
XX insecticidal protein; plant; pesticide; gene therapy;
KW lepidopteran insect pest; transgenic plant;
KW insect infestation resistance; monocol; dicot; cry1Bb; gene; ds.
XX
OS *Bacillus thuringiensis*.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 1241. .4933
FT CDS /tag= a
FT /product= "B thuringiensis cry1Bb variant protein"
XX
XX WO2004020636-A1.
XX
XX 11-MAR-2004.
XX
XX 26-AUG-2003; 2003WO-US026510.
XX
XX 29-AUG-2002; 2002US-0407428P.
XX
XX (MONS) MONSANTO TECHNOLOGY LLC.
PA (BOGD/) BOGDANOVA N N.
PA (ROMA/) ROMANO C P.
XX
XX Bogdanova NN, Romano CP;
XX
XX WPI; 2004-269221/25.
DR P-PSDB; ADK98489.
DR
XX
XX New polynucleotide sequence optimized for expression of an insecticidal
PT protein in a plant, useful in the control of Lepidoptera insect pests,
PT and for producing transgenic plants with the ability to resist insect
PT infestations.
XX
XX Claim 1; SEQ ID NO 11; 138pp; English.
XX
XX This invention relates to a novel polynucleotide sequence optimised for
CC expression of an insecticidal protein in a plant. The invention may be
CC useful for the production of pesticides whilst the disclosed sequences
CC may be used for gene therapy. The polynucleotide sequence and methods are
CC useful in the control of lepidopteran insect pests, and for producing
CC transgenic plants with the ability to resist insect infestations. The
CC invention provides polynucleotide sequences with enhanced, improved and
CC optimised expression in monocol and dicot plant species. The present
CC sequence is that of a B thuringiensis cry1Bb expression cassette which is
CC related to the invention.
XX
SQ Sequence 5170 BP; 1089 A; 1761 C; 1339 G; 981 T; 0 U; 0 Other;

Query Match 75.3%; Score 554; DB 12; Length 5170;
Best Local Similarity 94.5%; Pred. No. 7.8e-172;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

QY 116 TCTGACGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 28 TCCGATGTGAGACTTTTTCACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 87
QY 176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAGGAGTGGCACCTACAAATGCC 235
Db 88 CAGCTATCTGTCACTTATTGTGAAGATAGTGGAAAAAGGAGTGGCTCTCTACAAATGCC 147
QY 236 ATCATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGGTCCCAAAG 295
Db 148 ATCATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGGTCCCAAAG 207
QY 296 ATGGACCCCAACCCACGAGGAGCATCTGGAAGAAAGAGCTTCCAAACAGCTCTTCAA 355
Db 208 ATGGACCCCAACCCACGAGGAGCATCTGGAAGAAAGAGCTTCCAAACAGCTCTTCAA 267
QY 356 AGCAAGTGGATTGATGTGAT-----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
DT
XX

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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554	75.3	661	US-09-027-998A-33	Sequence 33, Appl
2	554	75.3	2107	US-09-441-340-29	Sequence 29, Appl
3	554	75.3	2122	US-09-441-340-25	Sequence 25, Appl
4	554	75.3	2436	US-09-441-340-31	Sequence 31, Appl
5	554	75.3	3469	US-09-377-466B-23	Sequence 23, Appl
6	554	75.3	3754	US-09-377-466B-15	Sequence 15, Appl
7	554	75.3	8012	US-09-182-117-1	Sequence 1, Appl
8	554	75.3	8012	US-09-434-039A-1	Sequence 1, Appl
9	554	75.3	8349	US-09-186-002-16	Sequence 16, Appl
10	554	75.3	8418	US-09-182-117-5	Sequence 5, Appl
11	554	75.3	8418	US-09-434-039A-5	Sequence 5, Appl
12	554	75.3	8798	US-09-182-117-4	Sequence 4, Appl
13	554	75.3	8798	US-09-434-039A-4	Sequence 4, Appl
14	551.4	74.9	1030	US-07-936-183-46	Sequence 46, Appl
15	551.4	74.9	1030	US-08-729-601A-43	Sequence 43, Appl
16	551.4	74.9	1196	US-08-729-601A-46	Sequence 46, Appl
17	551.4	74.9	5897	US-09-097-319A-26	Sequence 26, Appl
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20	550.4	74.8	9335	US-09-643-971-19	Sequence 19, Appl
21	550	74.7	10249	US-09-186-002-14	Sequence 14, Appl
22	550	74.7	10339	US-09-186-002-13	Sequence 13, Appl
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31	534.6	72.6	14446	4	US-09-810-861B-4	Sequence 4, Appl
32	526	71.5	12614	4	US-09-577-424-1	Sequence 1, Appl
33	514.4	69.9	10252	4	US-09-186-002-15	Sequence 15, Appl
34	505.6	68.7	5033	1	US-08-038-768A-1	Sequence 1, Appl
35	476.8	64.8	2728	3	US-08-836-402B-7	Sequence 7, Appl
36	459.2	62.4	1138	3	US-09-011-151-8	Sequence 8, Appl
37	459.2	62.4	1138	3	US-09-011-151-9	Sequence 9, Appl
38	459	62.4	1742	3	US-09-737-698B-30	Sequence 30, Appl
39	459	62.4	1742	3	US-09-737-626A-30	Sequence 30, Appl
40	459	62.4	1800	3	US-09-737-698B-29	Sequence 29, Appl
41	459	62.4	1800	4	US-09-737-626A-29	Sequence 29, Appl
42	366	49.7	907	4	US-09-623-551-17	Sequence 17, Appl
43	351.8	47.8	978	1	US-08-446-486-31	Sequence 31, Appl
44	351.8	47.8	978	1	US-08-463-308-31	Sequence 31, Appl
45	351.8	47.8	979	1	US-08-446-486-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-09-027-998A-33
; Sequence 33, Application US/09027998A
; Patent No. 6284949
; GENERAL INFORMATION:
; APPLICANT: Fischhoff, David A
; APPLICANT: Fuchs, Roy L
; APPLICANT: Perlak, Frederick J
; TITLE OF INVENTION: Insect Resistant Plants
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White and Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,998A
; FILING DATE: 23-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-09-027-998A-33

Query Match	75.3%	Score 554;	DB 3;	Length 661;
Best Local Similarity	94.5%	Pred. No. 7.8e-178;		
Matches 586;	Conservative 0;	Mismatches 30;	Indels 4;	Gaps 1;
Oy	116	TCTCAGTGAGACATTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCATTGCC	175	
Db	20	TCCGATGTGAGACATTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCATTGCC	79	
Oy	176	CAGTATCTGTCATTCATCAAAAGGACAGTAGAAAAGGAGGTGGACCTTACAAATGCC	235	

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Db      80 CAGCTATCTGTCACTTTATTGTGAGATAGTGGAAAGGAAGGTGGCTCTTACAAATGCC 139
Qy      236 ATCATTTCCGATAAAGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295
Db      140 ATCATTTCCGATAAAGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 199
Qy      296 ATGAGACCCCCACCACAGAGAGATCGTGGAAAGGAAGACGTTCCAAACCACTCTTCAA 355
Db      200 ATGAGACCCCCACCACAGAGAGATCGTGGAAAGGAAGACGTTCCAAACCACTCTTCAA 259
Qy      356 AGCAAGTGGATTGATGTGAT----TGCAGTCAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db      260 AGCAAGTGGATTGATGTGATGTCGATGTCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 319
Qy      412 AACCTCTCGGATTCCATTTGCCAGCTATCTGTCACTTTCATTCATCAAAAGGACAGTAGAAAAG 471
Db      320 AACCTCTCGGATTCCATTTGCCAGCTATCTGTCACTTTTATTTGGAAGATAGTGGAAAAG 379
Qy      472 GAAGTGGACCTACAAATGCCATCATTTGCGATAAAGGAAGGCTATCGTTCAAGATGCC 531
Db      380 GAAGTGGCTCTTCAAAATGCCATCATTTGCGATAAAGGAAGGCTATCGTTGAAGATGCC 439
Qy      532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAAGAGGACATCGTGGAAAAGAA 591
Db      440 TCTGCCGACAGTGGTCCCAAGATGGACCCCAAGAGGACATCGTGGAAAAGAA 499
Qy      592 GACGTTCCAAACCACTCTTCAAGCAAGTGGATGATGATATCTCCACTGACGTAAGG 651
Db      500 GACGTTCCAAACCACTCTTCAAGCAAGTGGATGATGATATCTCCACTGACGTAAGG 559
Qy      652 GATGACGCAATCCCACTATCTTCCGAAGACCTTCTCTATATAAGGAAGTTCATTT 711
Db      560 GATGACGCAATCCCACTATCTTCCGAAGACCTTCTCTATATAAGGAAGTTCATTT 619
Qy      712 CATTTGGAGGACACGCTG 731
Db      620 CATTTGGAGGACACGCTG 639
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RESULT 2

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US-09-441-340-29
; Sequence 29, Application US/09441340
; Patent No. 6448476
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/09/441.340
; CURRENT FILING DATE: 1999-11-16
; EARLIER APPLICATION NUMBER: 60/108,763
; EARLIER FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 2107
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:expression
; OTHER INFORMATION: cassette comprising plant operable promoter linked
; OTHER INFORMATION: to a leader, intron, a sequence encoding an AMPA
; OTHER INFORMATION: acetyltransferase, and termination sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (26)..(590)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (615)..(685)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (699)..(1148)
; FEATURE:
; NAME/KEY: transit_peptide
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; LOCATION: (1149)..(1426)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1427)..(1858)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (1869)..(2102)
US-09-441-340-29

Query Match      75.3%; Score 554; DB 3; Length 2107;
Best Local Similarity 94.5%; Pred. No. 1.5e-177;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy      116 TCTGCACTGAGACTTTTCAACAAAGGTAATATTCGGGAACCTCTCTCGGATTCATTCGCC 175
Db      28 TCCGATGTGAGACTTTTCAACAAAGGTAATATTCGGGAACCTCTCTCGGATTCATTCGCC 87
Qy      176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCACCTACAAATGCC 235
Db      88 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCTCTTACAAATGCC 147
Qy      236 ATCATTTCCGATAAAGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295
Db      148 ATCATTTCCGATAAAGAAAGGCTATCGTTGAAGATGCTCTGCCGACAGTGGTCCCAAAG 207
Qy      296 ATGGACCCCCACCACAGAGGACATCGTGGAAAAGGAAGACGTTCCAAACCACTCTTCAA 355
Db      208 ATGGACCCCCACCACAGAGGACATCGTGGAAAAGGAAGACGTTCCAAACCACTCTTCAA 267
Qy      356 AGCAAGTGGATTGATGTGAT---TGCAGTGGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db      268 AGCAAGTGGATTGATGTGATGTCGATGTCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 327
Qy      412 AACCTCTCGGATTCCATTTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAG 471
Db      328 AACCTCTCGGATTCCATTTGCCAGCTATCTGTCACTTTTATTTGGAAGATAGTGGAAAAG 387
Qy      472 GAAGTGGGACCTACAAATGCCATCATTTGCGATAAAGGAAGGCTATCGTTCAAGATGCC 531
Db      388 GAAGTGGGCTCTTACAAATGCCATCATTTGCGATAAAGGAAGGCTATCGTTGAAGATGCC 447
Qy      532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAAGAGGACATCGTGGAAAAGAA 591
Db      448 TCTGCCGACAGTGGTCCCAAGATGGACCCCAAGAGGACATCGTGGAAAAGAA 507
Qy      592 GACGTTCCAAACCACTCTTCAAGCAAGTGGATGATGATATCTCCACTGACGTAAGG 651
Db      508 GACGTTCCAAACCACTCTTCAAGCAAGTGGATGATGATATCTCCACTGACGTAAGG 567
Qy      652 GATGACGCAATCCCACTATCTTCCGAAGACCTTCTCTATATAAGGAAGTTCATTT 711
Db      568 GATGACGCAATCCCACTATCTTCCGAAGACCTTCTCTATATAAGGAAGTTCATTT 627
Qy      712 CATTTGGAGGACACGCTG 731
Db      628 CATTTGGAGGACACGCTG 647
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RESULT 3

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US-09-441-340-25
; Sequence 25, Application US/09441340
; Patent No. 6448476
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/09/441,340
; CURRENT FILING DATE: 1999-11-16
; EARLIER APPLICATION NUMBER: 60/108,763
; EARLIER FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
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472 GAAGGTGGCCACTACAAATGCCATTCATTGGATTAAGAAAGGATCGTTCAAGATGCC 531
Db
388 GAAGTGGCTCCTACAAATGCCATTCATTGGATTAAGAAAGGATCGTTGAAGATGCC 447
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAAGAGGAGCATCGTGGAAAAAGAA 591
Db 448 TCTGCCGACAGTGGTCCCAAGATGGACCCCAAGAGGAGCATCGTGGAAAAAGAA 507
Qy 592 GAGTTCACACCAAGTCTTCAAGCAAGTGGATGGATGATATCTCCACTGACGTAAGG 651
Db 508 GAGTTCACACCAAGTCTTCAAGCAAGTGGATGGATGATATCTCCACTGACGTAAGG 567
Qy 652 GATGACGACAAATCCCACTATCCTTCGCAAGACCTTCCTCTATATAAGGAAGTTCATTT 711
Db 568 GATGACGACAAATCCCACTATCCTTCGCAAGACCTTCCTCTATATAAGGAAGTTCATTT 627
Qy 712 CATTTGGAGAGGACACGCTG 731
Db 628 CATTTGGAGAGGACACGCTG 647
RESULT 5
US-09-377-466B-23
; Sequence 23, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 3469
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMv.35S
; NAME/KEY: 5'UTR
; LOCATION: (664)..(734)
; OTHER INFORMATION: L-Ta.hcb1
; NAME/KEY: intron
; LOCATION: (748)..(1238)
; OTHER INFORMATION: I-Os.Act1
; NAME/KEY: CDS
; LOCATION: (1241)..(3199)
; OTHER INFORMATION: Cry3Bb1 variant 11231mv2
; NAME/KEY: terminator
; LOCATION: (3217)..(3450)
; OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-23
Query Match 75.3%; Score 554; DB 4; Length 3469;
Best Local Similarity 94.5%; Pred. No. 2e-177;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTGCAGTGAAGCTTTTCAACAAGGGTAAATATCGGAAACCTTCCTCGGATTCATTGGCC 175
Db 28 TCCGATGTGAGACTTTTCACAAGGGTAAATATCCGAAACCTTCCTCGGATTCATTGGCC 87
Qy 176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAGGAGTGGCACCCTACAAATGCC 235
Db 88 CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAAGGAGTGGTCTCTACAAATGCC 147
Qy 236 ATCATTCGGATAAGGAAAGGCTATCGTTCAAGATGCTTCGGACAGTGGTCCCAAG 295
Db 148 ATCATTCGGATAAGGAAAGGCTATCGTTGAAGATGCTTCGCCGACAGTGGTCCCAAG 207

Qy 296 ATGAGCCCCCACCACGAGGAGCATCGTGGAAAAAGACGTTCCAAACACACGCTTCAA 355
Db 208 ATGAGCCCCCACCACGAGGAGCATCGTGGAAAAAGACGTTCCAAACACACGCTTCAA 267
Qy 356 AGCAAGTGGATTGATGTGAT- - - -TGCAGTGGAGACTTTTCAACAAAGGGTAAATATCGGGA 411
Db 268 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAAATATCGGGA 327
Qy 412 AACCTCTCGGATTCATTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
Db 328 AACCTCTCGGATTCATTGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 387
Qy 472 GAAGTGGCAGCTTACAAATGCCATATTCGATATAAGGAAAGGCTATCGTTCAAGATGCC 531
Db 388 GAAGTGGCTCTTACAAATGCCATATTCGATATAAGGAAAGGCTATCGTTGAAGATGCC 447
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAAGAGGAGCATCGTGGAAAAAGAA 591
Db 448 TCTGCCGACAGTGGTCCCAAGATGGACCCCAAGAGGAGCATCGTGGAAAAAGAA 507
Qy 592 GAGTTCACACCAAGTCTTCAAGCAAGTGGATGGATGATATCTCCACTGACGTAAGG 651
Db 508 GAGTTCACACCAAGTCTTCAAGCAAGTGGATGGATGATATCTCCACTGACGTAAGG 567
Qy 652 GATGACGACAAATCCCACTATCCTTCGCAAGACCTTCCTCTATATAAGGAAGTTCATTT 711
Db 568 GATGACGACAAATCCCACTATCCTTCGCAAGACCTTCCTCTATATAAGGAAGTTCATTT 627
Qy 712 CATTTGGAGAGGACACGCTG 731
Db 628 CATTTGGAGAGGACACGCTG 647
RESULT 6
US-09-377-466B-15
; Sequence 15, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 3754
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMv.35S
; NAME/KEY: intron
; LOCATION: (669)..(1472)
; OTHER INFORMATION: I-2m.Hsp70
; NAME/KEY: CDS
; LOCATION: (1490)..(3448)
; OTHER INFORMATION: Cry3Bb1 variant v11231
; NAME/KEY: terminator
; LOCATION: (3475)..(3730)
; OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
; OTHER INFORMATION: termination and polyadenylation sequence
US-09-377-466B-15
Query Match 75.3%; Score 554; DB 4; Length 3754;
Best Local Similarity 94.5%; Pred. No. 2.1e-177;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTGCAGTGAAGCTTTTCAACAAGGGTAAATATCGGAAACCTTCCTCGGATTCATTGGCC 175

Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAACCTCTCCGATTCATATGCC 87
Qy 176 CAGCTATCTGTCACCTTATCAAAAGGACAGTAGAAAAGAGGAGGCGACCTACAAATGCC 235
Db 88 CAGCTATCTGTCACCTTATTTGTAAGATAGTGGAAAGGAGGCTCTCTACAAATGCC 147
Qy 236 ATCAATGGGTAAGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTAGTGGTCCCAAAG 295
Db 148 ATCAATGGGTAAGAAAGGCTATCGTTGAAGATGCTCTGCGGACAGTAGTGGTCCCAAAG 207
Qy 296 ATGGACCCCAACACGAGGAGCTGTTGGAAAGAGAGGCTTCCAAACACAGCTTTCAA 355
Db 208 ATGGACCCCAACACGAGGAGCTGTTGGAAAGAGAGGCTTCCAAACACAGCTTTCAA 267
Qy 356 AGCAAGTGGATGTGATGAT----TGCAAGTGGAGCTTTTCAACAAAGGGTAATATCCGGA 411
Db 268 AGCAAGTGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 327
Qy 412 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAG 471
Db 328 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTTATTTGTAAGATAGTGGAAAG 387
Qy 472 GAAGTGGCACTACAAATGCCATCATTTGCGATAAAGGAGGCTATCGTTCAAGATGCC 531
Db 388 GAAGTGGCTCTACAAATGCCATCATTTGCGATAAAGGAGGCTATCGTTGAAGATGCC 447
Qy 532 TCTGCCGACAGTGGTCCAAAGATGGACCCCAACGAGGAGCATCGTGGAAAAAGAA 591
Db 448 TCTGCCGACAGTGGTCCAAAGATGGACCCCAACGAGGAGCATCGTGGAAAAAGAA 507
Qy 592 GACGTTCCAAACACGCTCTTCAAGCAAGTGAATGATGATGATGATGATGATGATGATGAT 651
Db 508 GACGTTCCAAACACGCTCTTCAAGCAAGTGAATGATGATGATGATGATGATGATGATGAT 567
Qy 652 GATGCGCACATCCCACTATCTTCCGACAGCCTTCTCTATATAGGAAGTTCATTT 711
Db 568 GATGCGCACATCCCACTATCTTCCGACAGCCTTCTCTATATAGGAAGTTCATTT 627
Qy 712 CATTGGAGAGGACACGCTG 731
Db 628 CATTGGAGAGGACACGCTG 647

RESULT 7

US-09-182-117-1
; Sequence 1, Application US/09182117
; Patent No. 6204436
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic Plant
; NUMBER OF SEQUENCES: 27
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/182,117
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8012 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-182-117-1

Query Match 75.3%; Score 554; DB 3; Length 8012;
Best Local Similarity 94.5%; Pred. No. 3.3e-177;

Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTCAGTGAAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATATGCC 175
Db 3044 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCTGGATTCATATGCC 3103
Qy 176 CAGCTATCTGTCACCTTATCAAAAGGACAGTAGAAAAGAGGCTTCCAAATGCC 235
Db 3104 CAGCTATCTGTCACCTTATTTGTAAGATAGTGGAAAGGAGGCTCTCTACAAATGCC 3163
Qy 236 ATCAATGGGTAAGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTAGTGGTCCCAAAG 295
Db 3164 ATCAATGGGTAAGAAAGGCTATCGTTGAAGATGCTCTGCGGACAGTAGTGGTCCCAAAG 3223
Qy 296 ATGGACCCCAACACGAGGAGCATCGTGGAAAGAGAGGCTTCCAAACACAGCTTTCAA 355
Db 3224 ATGGACCCCAACACGAGGAGCATCGTGGAAAGAGAGGCTTCCAAACACAGCTTTCAA 3283
Qy 356 AGCAAGTGGATGTGATGAT----TGCAAGTGGAGCTTTTCAACAAAGGGTAATATCCGGA 411
Db 3284 AGCAAGTGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3343
Qy 412 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAG 471
Db 3344 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTTATTTGTAAGATAGTGGAAAG 3403
Qy 472 GAAGTGGCACTACAAATGCCATCATTTGCGATAAAGGAGGCTATCGTTCAAGATGCC 531
Db 3404 GAAGTGGCTCTTACAAATGCCATCATTTGCGATAAAGGAGGCTATCGTTGAAGATGCC 3463
Qy 532 TCTGCCGACAGTGGTCCAAAGATGGACCCCAACGAGGAGCATCGTGGAAAAAGAA 591
Db 3464 TCTGCCGACAGTGGTCCAAAGATGGACCCCAACGAGGAGCATCGTGGAAAAAGAA 3523
Qy 592 GACGTTCCAAACACGCTCTTCAAGCAAGTGAATGATGATGATGATGATGATGATGATGAT 651
Db 3524 GACGTTCCAAACACGCTCTTCAAGCAAGTGAATGATGATGATGATGATGATGATGATGAT 3583
Qy 652 GATGCGCACATCCCACTATCTTCCGACAGCCTTCTCTATATAGGAAGTTCATTT 711
Db 3584 GATGCGCACATCCCACTATCTTCCGACAGCCTTCTCTATATAGGAAGTTCATTT 3643
Qy 712 CATTGGAGAGGACACGCTG 731
Db 3644 CATTGGAGAGGACACGCTG 3663

RESULT 8

US-09-434-039A-1
; Sequence 1, Application US/09434039A
; Patent No. 6531649
; GENERAL INFORMATION:
; APPLICANT: MANNERLOEF, Marie
; APPLICANT: TENNING, Paul Peter
; APPLICANT: STEEN, Per
; TITLE OF INVENTION: Transgenic Plants
; FILE REFERENCE: 09/434,039
; CURRENT APPLICATION NUMBER: US/09/434,039A
; CURRENT FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/112,003
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 09/182,117
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 8012
; TYPE: DNA
; ORGANISM: Sugar beet
US-09-434-039A-1

Query Match 75.3%; Score 554; DB 4; Length 8012;
Best Local Similarity 94.5%; Pred. No. 3.3e-177;

Matches	586;	Conservative	0;	Mismatches	30;	Indels	4;	Gaps	1;
Qy	116	TCTGCAGT	GTAGAC	TTTTCAACAAAGGGT	TAATATATCGGAAACCTCTCGGAT	TCCATTG	CC	175	
Db	3044	TCCGATGTGAGAC	TTTTCAACAAAGGGT	TAATATCGGAAACCTCTCGGAT	TCCATTG	CC	3103		
Qy	176	CAGCTATCTGTCACTT	CATCAAAGGACAGT	AGAAAAGGAAGGTGG	CACCTCACAAAATG	CC	235		
Db	3104	CAGCTATCTGTCACTT	TAATGTGAAGATAGTGG	AAAAAGGAAGGTGGCTCTCTACAAATG	CC	3163			
Qy	236	ATCAATTCGGATAAAG	GAAGGCTATCGTTCAAGATG	CTCTGCGGACAGATGGT	CTCCCAAAG	295			
Db	3164	ATCAATTCGGATAAAG	GAAGGCTATCGTTCAAGATG	CTCTGCGGACAGATGGT	CTCCCAAAG	3223			
Qy	296	ATGGACCCCCCA	CCACGAGGAGCATCGTGG	AAAAAAGAAAGAGCTT	CCAAACCAACG	CTTCAA	355		
Db	3224	ATGGACCCCCCA	CCACGAGGAGCATCGTGG	AAAAAAGAAAGAGCTT	CCAAACCAACG	CTTCAA	3283		
Qy	356	AGCAAGTGGAT	TGATGTGAT	-----TGCAAGT	GTAGACTTTCAACAAGGGT	TAATATCGGA	411		
Db	3284	AGCAAGTGGAT	TGATGTGATGTG	ATGCGATGCGGATG	GAGACTTTTCAACAAGGGT	TAATATCGGA	3343		
Qy	412	AACCTCTCGGAT	TCCTATGTC	CCAGCTATCTGTCACTT	CAATCAAAAGGACAGT	AGAAAG	471		
Db	3344	AACCTCTCGGAT	TCCTATGTC	CCAGCTATCTGTCACTT	ATGGAAGATAGTGA	AAAG	3403		
Qy	472	GAAGGTGGC	ACCTCAAAATGCC	ATCATTCGATAAAGGAAGG	CTATCGTTCAAGAT	CC	531		
Db	3404	GAAGGTGGCT	CCTCAAAATGCCATCAT	TGCGATTAAGGAAGG	CCATCGTTGAAGAT	CC	3463		
Qy	532	TCTGCCGACAGT	TGGTCTCCAAAGAT	GGACCCCAACGAGGAG	GCATCGTGGAAAAAGAA	591			
Db	3464	TCTGCCGACAGT	TGGTCTCCAAAGAT	GGACCCCAACGAGGAG	GCATCGTGGAAAAAGAA	3523			
Qy	592	GACGTTTCCAA	CCACCGTCTTCAAAGCAAGT	GGATGTGATATCTCCATG	ACGTGAAGG	651			
Db	3524	GACGTTTCCAA	CCACCGTCTTCAAAGCAAGT	GGATGTGATATCTCCATG	ACGTGAAGG	3583			
Qy	652	GATGAGCGCAA	TCCCCACTATC	CTTCCCAAGACCCCTT	CCTCTATATGAAG	GAAGTTCA	711		
Db	3584	GATGAGCGCA	NATCCCCACTATC	CTTCCCAAGACCCCTT	CCTCTATATGAAG	GAAGTTCA	3643		
Qy	712	CATTGAGAGG	ACACGCTG	731					
Db	3644	CATTGAGAGG	ACACGCTG	3663					

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RESULT 9
US-09-186-002-16
; Sequence 16, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; TITLE OF INVENTION: delta-Endocoxins
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 8349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3666)..(5573)
; OTHER INFORMATION: completely synthesized
US-09-186-002-16

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Query Match	75.3%;	Score 554;	DB 4;	Length 8349;
Best Local Similarity	94.5%;	Pred. No. 3.3e-177;		

	Matches	586;	Conservative	0;	Mismatches	30;	Indels	4;	Gaps	1;
QY	116	TCTCAGTGGAGACTTTTCAACAAAGGTAATATCGGGAACCCTCTCGGATTCATTGCC	175							
Db	1807	TCCGATGTGAGACTTTTCAACAAAGGTAATATCCGGAACCTCTCTCGGATTCATTGCC	1866							
QY	176	CAGCTATCTGTCACTTTCATCAAAGGCAGTGAGAAGAAGGTGGCACCTCAAAATGCC	235							
Db	1867	CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAGAAGGAGGTGGCTCTCAAAAATGCC	1926							
QY	236	ATCATTCGGATAAAGGAAGGCTATCGTTCAGATGCTCTGCCGACAGTGGTCCCAAAG	295							
Db	1927	ATCATTCGGATAAAGGAAGGCCATCGTTGAAGATGCCTCTGCCACAGTGGTCCCAAAG	1986							
QY	296	ATGACCCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACACACGCTTTCAA	355							
Db	1987	ATGACCCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACACGCTTTCAA	2046							
QY	356	AGCAAGTGGATTGATGTGAT-----TGCAGTGAACATTTTCAACAAGGGTAAATATCGGA	411							
Db	2047	AGCAAGTGGATTGATGTGATGTGGTCCGATGTGAGACTTTTCAACAAGGGTAAATATCGGA	2106							
QY	412	AACCTCTCTCGAATTCATTGCCACAGTATCTGTCACTTCATTCAAAAGGACAGTAGAAAAAG	471							
Db	2107	AACCTCTCTCGAATTCATTGCCACAGTATCTGTCACTTCATTCTGAAGATAGTGGAAAAAG	2166							
QY	472	GAAGGTGGACCTTCAAAATGCCATCATTTGGATAAAGGAAAGGCTATCGTTCAAGATGCC	531							
Db	2167	GAAGGTGGCTCTCTCAAAATGCCATCATTTGGATAAAGGAAAGGCCATCGTTGAAGATGCC	2226							
QY	532	TCTGCCACAGTGGTGTCCAAAGATGGACCCCACACGAGGAGCATCGTGGAAAAAGAA	591							
Db	2227	TCTGCCACAGTGGTGTCCAAAGATGGACCCCACACGAGGAGCATCGTGGAAAAAGAA	2286							
QY	592	GAGGTTCCAACCAAGCTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG	651							
Db	2287	GAGGTTCCAACCAAGCTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG	2346							
QY	652	GATGACCCACAATCCCACTATCTCTCGCAAGACCCCTTCTCTATATAAGGAAGTTCATTT	711							
Db	2347	GATGACCCACAATCCCACTATCTCTTCCGAAGACCCCTTCTCTATATAAGGAAGTTCATTT	2406							
QY	712	CATTGGAGGACACGCTG	731							
Db	2407	CATTGGAGGACACGCTG	2426							

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RESULT 10
US-09-182-117-5
; Sequence 5, Application US/09182117
; Patent No. 6204436
; GENERAL INFORMATION:
;   APPLICANT:
;   TITLE OF INVENTION: Transgenic Plant
;   NUMBER OF SEQUENCES: 27
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/182,117
;   FILING DATE:
;   CLASSIFICATION:
;   INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 8418 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO

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US-09-182-117-5

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Query Match      75.3%; Score 554; DB 3; Length 8418;
Best Local Similarity 94.5%; Pred. No. 3.4e-177;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGAGTGTGAGCTTTTCAACAAAGGGTAATATCGGGAAACCTCTCGGATTCATTTGCC 175
Db 3023 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTCGGATTCATTTGCC 3082

Qy 176 CAGCTATCTGTCACTTTTCAACAAAGGACAGTAGAAGAGGAGGTGGACCTTACAAATGCC 235
Db 3083 CAGCTATCTGTCACTTTTCAACAAAGGACAGTAGAAGAGGAGGTGGCTCTTACAAATGCC 3142

Qy 236 ATCATTTCCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295
Db 3143 ATCATTTCCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 3202

Qy 296 ATGGACCCCAACCCACGAGGAGCATCGTTGGAAAAAGAAAGAGCTTTCCAAACCAAGCTTTCAA 355
Db 3203 ATGGACCCCAACCCACGAGGAGCATCGTTGGAAAAAGAAAGAGCTTTCCAAACCAAGCTTTCAA 3262

Qy 356 AGCAAGTGGATTGATGTGAT---TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 3263 AGCAAGTGGATTGATGTGATGTGCTCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 3322

Qy 412 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAG 471
Db 3323 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTATTGTGCAAGATAGTGGAAAAAG 3382

Qy 472 GAAGTGGCACTTACAAATGCCATTCATTTGGGATAAAGAAAGGCTATCGTTCAAGATGCC 531
Db 3383 GAAGTGGCTCTCTACAAATGCCATTCATTTGGGATAAAGAAAGGCTATCGTTGAAAGATGCC 3442

Qy 532 TCTGCCGACAGTGGTCCCAAGAGTGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 591
Db 3443 TCTGCCGACAGTGGTCCCAAGAGTGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 3502

Qy 592 GACGTTTCAACCAACCGCTCTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 651
Db 3503 GACGTTTCAACCAACCGCTCTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 3562

Qy 652 GATGAGCACAATCCCACTATCTTTCGCAAGACCCCTTCTCTATATAAGGAAGTTCAATTT 711
Db 3563 GATGAGCACAATCCCACTATCTTTCGCAAGACCCCTTCTCTATATAAGGAAGTTCAATTT 3622

Qy 712 CATTTGGAGAGGACACGCTG 731
Db 3623 CATTTGGAGAGGACACGCTG 3642
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RESULT 11

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US-09-434-039A-5
; Sequence 5, Application US/09434039A
; Patent No. 6531649
; GENERAL INFORMATION:
; APPLICANT: MANNERLOEF, Marie
; APPLICANT: TENNING, Paul Peter
; APPLICANT: STEEN, Per
; TITLE OF INVENTION: Transgenic Plants
; FILE REFERENCE: 09/434,039
; CURRENT APPLICATION NUMBER: US/09/434,039A
; CURRENT FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/112,003
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 09/182,117
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 8418
; TYPE: DNA
; ORGANISM: Sugar beet
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US-09-434-039A-5

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Query Match      75.3%; Score 554; DB 4; Length 8418;
Best Local Similarity 94.5%; Pred. No. 3.4e-177;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGAGTGTGAGCTTTTCAACAAAGGGTAATATCGGGAAACCTCTCGGATTCATTTGCC 175
Db 3023 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTCGGATTCATTTGCC 3082

Qy 176 CAGCTATCTGTCACTTTTCAACAAAGGACAGTAGAAGAGGAGGTGGACCTTACAAATGCC 235
Db 3083 CAGCTATCTGTCACTTTTCAACAAAGGACAGTAGAAGAGGAGGTGGCTCTTACAAATGCC 3142

Qy 236 ATCATTTCCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295
Db 3143 ATCATTTCCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 3202

Qy 296 ATGGACCCCAACCCACGAGGAGCATCGTTGGAAAAAGAAAGAGCTTTCCAAACCAAGCTTTCAA 355
Db 3203 ATGGACCCCAACCCACGAGGAGCATCGTTGGAAAAAGAAAGAGCTTTCCAAACCAAGCTTTCAA 3262

Qy 356 AGCAAGTGGATTGATGTGAT---TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 3263 AGCAAGTGGATTGATGTGATGTGCTCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 3322

Qy 412 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAG 471
Db 3323 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTATTGTGCAAGATAGTGGAAAAAG 3382

Qy 472 GAAGTGGCACTTACAAATGCCATTCATTTGGGATAAAGAAAGGCTATCGTTCAAGATGCC 531
Db 3383 GAAGTGGCTCTCTACAAATGCCATTCATTTGGGATAAAGAAAGGCTATCGTTGAAAGATGCC 3442

Qy 532 TCTGCCGACAGTGGTCCCAAGAGTGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 591
Db 3443 TCTGCCGACAGTGGTCCCAAGAGTGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 3502

Qy 592 GACGTTTCAACCAACCGCTCTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 651
Db 3503 GACGTTTCAACCAACCGCTCTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 3562

Qy 652 GATGAGCACAATCCCACTATCTTTCGCAAGACCCCTTCTCTATATAAGGAAGTTCAATTT 711
Db 3563 GATGAGCACAATCCCACTATCTTTCGCAAGACCCCTTCTCTATATAAGGAAGTTCAATTT 3622

Qy 712 CATTTGGAGAGGACACGCTG 731
Db 3623 CATTTGGAGAGGACACGCTG 3642
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RESULT 12

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US-09-182-117-4
; Sequence 4, Application US/09182117
; Patent No. 6204436
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic Plant
; NUMBER OF SEQUENCES: 27
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/182,117
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8798 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-182-117-4

Query Match      75.3%; Score 554; DB 3; Length 8798;
Best Local Similarity 94.5%; Pred. No. 3.4e-177;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCAGTGAGACTTTTCAACAAAGGGTAATATATCGGAAACCTCTCGGATTCATTTGCC 175
Db 3133 TCCGATGTGAGACTTTTCAACAAAGGGTAATATATCGGAAACCTCTCGGATTCATTTGCC 3192

Qy 176 CAGCTATCTGTCACTTCAATCAAAAGGACAGTAGAAAAAGGAAGGTGGCACCTACAAATGCC 235
Db 3193 CAGCTATCTGTCACTTATTTGTGAAGATAGTGGAAAAAGGAAGGTGGCTCTACAAATGCC 3252

Qy 236 ATCAATTGGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295
Db 3253 ATCAATTGGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 3312

Qy 296 ATGACCCCCACCCACGAGGAGCATCGTGGAAAAAGGAAGAGCTTTCCAAACCAAGTCTTCAA 355
Db 3313 ATGACCCCCACCCACGAGGAGCATCGTGGAAAAAGGAAGAGCTTTCCAAACCAAGTCTTCAA 3372

Qy 356 AGCAAGTGGATTGATGTGAT-----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 3373 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 3432

Qy 412 AACCTCTCGGATTCCTATGCCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAG 471
Db 3433 AACCTCTCGGATTCCTATGCCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAG 3492

Qy 472 GAAGGTGGACCTACAAATGCCATTCATTCGATATAAGAAAGGCTATCGTTCAAGATGCC 531
Db 3493 GAAGGTGGCTCTACAAATGCCATTCATTCGATATAAGAAAGGCTATCGTTCAAGATGCC 3552

Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAAGGAGGAGGAGCATCGTGGAAAAAGAA 591
Db 3553 TCTGCCGACAGTGGTCCCAAGATGGACCCCAAGGAGGAGGAGCATCGTGGAAAAAGAA 3612

Qy 592 GACGTTCCAAACCAAGTCTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 651
Db 3613 GACGTTCCAAACCAAGTCTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 3672

Qy 652 GATGACGACAAATCCCACTATCTTTCGCAAGAGCCCTTCTCTATATAAGGAAGTTCATTT 711
Db 3673 GATGACGACAAATCCCACTATCTTTCGCAAGAGCCCTTCTCTATATAAGGAAGTTCATTT 3732

Qy 712 CATTTGGAGGAGCACGCTG 731
Db 3733 CATTTGGAGGAGCACGCTG 3752
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RESULT 13

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US-09-434-039A-4
; Sequence 4, Application US/09434039A
; Patent No. 6531649
; GENERAL INFORMATION:
; APPLICANT: MANNERLOEF, Marie
; APPLICANT: TENNING, Paul Peter
; APPLICANT: STEEN, Per
; TITLE OF INVENTION: Transgenic Plants
; FILE REFERENCE: 09/434,039
; CURRENT APPLICATION NUMBER: US/09/434,039A
; CURRENT FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/112,003
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 09/182,117
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 4
; LENGTH: 8798
; TYPE: DNA
; ORGANISM: Sugar beet
US-09-434-039A-4

Query Match      75.3%; Score 554; DB 4; Length 8798;
Best Local Similarity 94.5%; Pred. No. 3.4e-177;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCAGTGAGACTTTTCAACAAAGGGTAATATATCGGAAACCTCTCGGATTCATTTGCC 175
Db 3133 TCCGATGTGAGACTTTTCAACAAAGGGTAATATATCGGAAACCTCTCGGATTCATTTGCC 3192

Qy 176 CAGCTATCTGTCACTTCAATCAAAAGGACAGTAGAAAAAGGAAGGTGGCACCTACAAATGCC 235
Db 3193 CAGCTATCTGTCACTTATTTGTGAAGATAGTGGAAAAAGGAAGGTGGCTCTACAAATGCC 3252

Qy 236 ATCAATTGGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295
Db 3253 ATCAATTGGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 3312

Qy 296 ATGACCCCCACCCACGAGGAGCATCGTGGAAAAAGGAAGAGCTTTCCAAACCAAGTCTTCAA 355
Db 3313 ATGACCCCCACCCACGAGGAGCATCGTGGAAAAAGGAAGAGCTTTCCAAACCAAGTCTTCAA 3372

Qy 356 AGCAAGTGGATTGATGTGAT-----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 3373 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 3432

Qy 412 AACCTCTCGGATTCCTATGCCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAG 471
Db 3433 AACCTCTCGGATTCCTATGCCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAG 3492

Qy 472 GAAGGTGGACCTACAAATGCCATTCATTCGATATAAGAAAGGCTATCGTTCAAGATGCC 531
Db 3493 GAAGGTGGCTCTACAAATGCCATTCATTCGATATAAGAAAGGCTATCGTTCAAGATGCC 3552

Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAAGGAGGAGGAGCATCGTGGAAAAAGAA 591
Db 3553 TCTGCCGACAGTGGTCCCAAGATGGACCCCAAGGAGGAGGAGCATCGTGGAAAAAGAA 3612

Qy 592 GACGTTCCAAACCAAGTCTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 651
Db 3613 GACGTTCCAAACCAAGTCTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 3672

Qy 652 GATGACGACAAATCCCACTATCTTTCGCAAGAGCCCTTCTCTATATAAGGAAGTTCATTT 711
Db 3673 GATGACGACAAATCCCACTATCTTTCGCAAGAGCCCTTCTCTATATAAGGAAGTTCATTT 3732

Qy 712 CATTTGGAGGAGCACGCTG 731
Db 3733 CATTTGGAGGAGCACGCTG 3752
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RESULT 14

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US-07-936-163-46
; Sequence 46, Application US/07936163
; Patent No. 5743477
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: MERLO, DONALD J
; APPLICANT: HOUTCHENS, ROBERT A
; APPLICANT: STRICKLAND, JAMES A
; APPLICANT: ORR, GREGORY L
; TITLE OF INVENTION: INSECTICIDAL PROTEINS AND METHOD FOR
; TITLE OF INVENTION: PLANT PROTECTION
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS D. ZINDRICK
; STREET: 9002 PURDUE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
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COUNTRY: US
ZIP: 46268-1189
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/936,163
FILING DATE: 27-AUG-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ZINDRICK, THOMAS D
REGISTRATION NUMBER: 32,185
REFERENCE/DOCKET NUMBER: C-38,424A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-1869
INFORMATION FOR SEQ ID NO: 46:
LENGTH: 1030 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-936-163-46

Query Match 74.9%; Score 551.4; DB 1; Length 1030;
Best Local Similarity 93.2%; Pred. No. 7.7e-177;
Matches 588; Conservative 0; Mismatches 41; Indels 2; Gaps 1;

Qy	105	CTGCAGAGCTTCTGCAGTGAGACTTTTCAACAAGGGTAAATATCGGGAACCTCTCGG	164
Db	13	CTGCAGATCTGCATGGGTGGAGACTTTTCAACAAGGGTAAATATCGGGAACCTCTCGG	72
Qy	165	ATTCATTTGCCAGCTATCTGCTACTTTCATCAAAAGGACAGTAGAAAAGGAAGTGGCAC	224
Db	73	ATTCATTTGCCAGCTATCTGCTACTTATGTGAAGATAGTGAAGAGGAGTGGCTC	132
Qy	225	CTACAAATGCCATCATTTGCCGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAG	284
Db	133	CTACAAATGCCATCATTTGCCGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAG	192
Qy	285	TGGTCCCAAGATGGACCCCAACCCACGAGAGCATCGTGGAAAAGAACGTTCCAAC	344
Db	193	TGGTCCCAAGATGGACCCCAACCCACGAGAGCATCGTGGAAAAGAACGTTCCAAC	252
Qy	345	CACGTCTTCAAGCAAGTGGATTGATGTGAT--TGCAAGTGAAGCTTTTCAACAAGGGTA	402
Db	253	CACGTCTTCAAGCAAGTGGATTGATGTGATCATCATGATGAGACTTTTCAACAAGGGTA	312
Qy	403	ATATCGGAAACCTCTCGGATTCATTTGCCAGTATCGTTGCCAGCTATCTGTCAATCAAAAGACA	462
Db	313	ATATCGGAAACCTCTCGGATTCATTTGCCAGTATCGTTGCCAGCTATCTGTCAATCAATGAATA	372
Qy	463	GTAGAAAAGGAAGTGGCACCCTACAAATGCCATTCGATTAAGGAAGGCTATCGTT	522

RESULT 15
US-08-729-601A-43
Sequence 43, Application US/08729601A
Patent No. 6166302
GENERAL INFORMATION:
APPLICANT: Merlo, Donald J.
APPLICANT: Folkerts, Otto
TITLE OF INVENTION: Modified Bacillus Thuringiensis Gene for
TITLE OF INVENTION: Lepidopteran Control in Plants
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle St.
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/729,601A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Krueger, James P.
REGISTRATION NUMBER: 35,234
REFERENCE/DOCKET NUMBER: 60089
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
TELEFAX: 312-372-7848
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1030 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-729-601A-43

Query Match 74.9%; Score 551.4; DB 3; Length 1030;
Best Local Similarity 93.2%; Pred. No. 7.7e-177;
Matches 588; Conservative 0; Mismatches 41; Indels 2; Gaps 1;

Qy	105	CTGCAGAGCTTCTGCAGTGAGACTTTTCAACAAGGGTAAATATCGGGAACCTCTCGG	164
Db	13	CTGCAGATCTGCATGGGTGGAGACTTTTCAACAAGGGTAAATATCGGGAACCTCTCGG	72
Qy	165	ATTCATTTGCCAGCTATCTGCTACTTTCATCAAAAGGACAGTAGAAAAGGAAGTGGCAC	224
Db	73	ATTCATTTGCCAGCTATCTGCTACTTATGTGAAGATAGTGAAGAGGAGTGGCTC	132
Qy	225	CTACAAATGCCATCATTTGCCGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAG	284
Db	133	CTACAAATGCCATCATTTGCCGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAG	192
Qy	285	TGGTCCCAAGATGGACCCCAACCCACGAGAGCATCGTGGAAAAGAACGTTCCAAC	344
Db	193	TGGTCCCAAGATGGACCCCAACCCACGAGAGCATCGTGGAAAAGAACGTTCCAAC	252
Qy	345	CACGTCTTCAAGCAAGTGGATTGATGTGAT--TGCAAGTGAAGCTTTTCAACAAGGGTA	402
Db	253	CACGTCTTCAAGCAAGTGGATTGATGTGATCATCATGATGAGACTTTTCAACAAGGGTA	312
Qy	403	ATATCGGAAACCTCTCGGATTCATTTGCCAGTATCGTTGCCAGCTATCTGTCAATCAAAAGACA	462
Db	313	ATATCGGAAACCTCTCGGATTCATTTGCCAGTATCGTTGCCAGCTATCTGTCAATCAATGAATA	372
Qy	463	GTAGAAAAGGAAGTGGCACCCTACAAATGCCATTCGATTAAGGAAGGCTATCGTT	522

Db	373	GTGAAAAGGAAGGTGGCTCTACAAATGCCATCATTTGCGATAAAGGAAGGCCATCGTT	432
Qy	523	CAAGATGCTCTGCGACAGTGTCCCAAGATGGACCCACCCACGAGGAGCATCGTG	582
Db	433	GAAGATGCTCTGCGACAGTGTCCCAAGATGGACCCACCCACGAGGAGCATCGTG	492
Qy	583	GAAAAGAAGACGTTCCAAACCACGCTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACT	642
Db	493	GAAAAGAAGACGTTCCAAACCACGCTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACT	552
Qy	643	GACGTAAGGGATGACGACACATCCCACTATCTTCGCAAGACCCCTTCCTCTATATAAGGA	702
Db	553	GACGTAAGGGATGACGACACATCCCACTATCTTCGCAAGACCCCTTCCTCTATATAAGGA	612
Qy	703	AGTTCAATTCATTGGAGGACACGCTGGA	733
Db	613	AGTTCAATTCATTGGAGGACACGCTGGA	643

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Job time : 186 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 12:54:20 ; Search time 718 Seconds
(without alignments)
7139.448 Million cell updates/sec

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Perfect score: 736
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Scoring table: IDENTITY NUC
Gapop 10'0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues
Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
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26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	597.4	81.2	1360	22	US-10-075-105C-3 Sequence 3, Appli
3	554	75.3	661	9	US-09-943-692-33 Sequence 33, Appl
4	554	75.3	2107	15	US-10-213-791-29 Sequence 29, Appl
5	554	75.3	2122	15	US-10-213-791-25 Sequence 25, Appl
6	554	75.3	2436	15	US-10-213-791-31 Sequence 31, Appl
7	554	75.3	3469	15	US-10-232-665-23 Sequence 23, Appl

8	554	75.3	3754	15	US-10-232-665-15	Sequence 15, Appl
9	554	75.3	8349	16	US-10-198-478-16	Sequence 16, Appl
c 10	551.4	74.9	5796	17	US-10-378-810-2	Sequence 2, Appli
11	551.4	74.9	5897	19	US-10-759-602-26	Sequence 26, Appl
12	550.4	74.8	9335	19	US-10-759-602-19	Sequence 19, Appl
13	550	74.7	10249	16	US-10-198-478-14	Sequence 14, Appl
14	550	74.7	10312	16	US-10-198-478-15	Sequence 15, Appl
15	550	74.7	10339	16	US-10-198-478-13	Sequence 13, Appl
16	548.4	74.5	10160	19	US-10-759-602-8	Sequence 8, Appli
17	548.4	74.5	11784	19	US-10-759-602-9	Sequence 9, Appli
18	548.4	74.5	11991	19	US-10-759-602-10	Sequence 10, Appl
19	543.6	73.9	4149	15	US-10-232-665-13	Sequence 13, Appl
20	534.6	72.6	5767	9	US-09-810-861B-3	Sequence 3, Appli
21	534.6	72.6	5767	22	US-10-792-491-3	Sequence 4, Appli
22	534.6	72.6	14446	9	US-09-810-861B-4	Sequence 4, Appli
23	534.6	72.6	14446	22	US-10-792-491-4	Sequence 4, Appli
24	526	71.5	829	14	US-10-109-812-10	Sequence 10, Appl
25	526	71.5	1334	16	US-10-322-656-12	Sequence 12, Appl
c 26	526	71.5	11478	21	US-10-473-945-2	Sequence 2, Appli
27	526	71.5	12304	21	US-10-473-945-5	Sequence 5, Appli
c 28	526	71.5	12497	21	US-10-473-945-4	Sequence 4, Appli
c 29	514	69.8	8428	15	US-10-161-403-90	Sequence 90, Appl
c 30	514	69.8	8428	20	US-10-161-408-2	Sequence 2, Appli
c 31	514	69.8	8428	24	US-11-006-076-90	Sequence 90, Appl
c 32	514	69.8	10122	15	US-10-161-403-97	Sequence 97, Appl
c 33	514	69.8	10122	20	US-10-161-408-8	Sequence 8, Appli
c 34	514	69.8	10122	24	US-11-006-076-97	Sequence 97, Appl
c 35	514	69.8	10549	15	US-10-161-403-92	Sequence 92, Appl
c 36	514	69.8	10549	20	US-10-161-408-3	Sequence 3, Appli
c 37	514	69.8	10549	24	US-11-006-076-92	Sequence 92, Appl
c 38	514	69.8	11182	15	US-10-161-403-89	Sequence 89, Appl
c 39	514	69.8	11182	15	US-10-161-403-89	Sequence 89, Appl
c 40	514	69.8	11182	20	US-10-161-408-1	Sequence 1, Appli
c 41	514	69.8	11182	20	US-10-161-408-1	Sequence 1, Appli
c 42	514	69.8	11182	24	US-11-006-076-89	Sequence 89, Appl
c 43	514	69.8	11182	24	US-11-006-076-89	Sequence 89, Appl
c 44	514	69.8	12592	15	US-10-161-403-95	Sequence 95, Appl
c 45	514	69.8	12592	15	US-10-161-403-95	Sequence 95, Appl

ALIGNMENTS

RESULT 1
US-10-075-105C-1
; Sequence 1, Application US/10075105C
; Publication No. US20050188432A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zhijian T
; TITLE OF INVENTION: Bi-Directional Dual Promoter Complex with Enhanced Promoter Activ
; TITLE OF INVENTION: Transgene Expression in Eukaryotes
; FILE REFERENCE: 7270-72978
; CURRENT APPLICATION NUMBER: US/10/075.105C
; PRIOR FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/268,358
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 736
; TYPE: DNA
; ORGANISM: CamV 35S
; FEATURE:
; OTHER INFORMATION:
US-10-075-105C-1

Query Match 100.0%; Score 736; DB 22; Length 736;
Best Local Similarity 100.0%; Pred. No. 1.5e-238;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGATCCAGCGTGTCTCTCCAAATCAATCAATCTTATATAGAGAGGCTCTGCCG 60
|||||

Db 1 GGATCCAGCGTGCTCTCCAAATGAAATGAATCTTCTTATATAGAGGAAGGCTTTGGC 60
Qy 61 AAGGATAGTGGGATTGTGCGTCATCCCTTACGTTCAGTGGAGATATCTCGAAGCTTCTGC 120
Db 61 AAGGATAGTGGGATTGTGCGTCATCCCTTACGTTCAGTGGAGATATCTCGAAGCTTCTGC 120
Qy 121 AGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCCATTGCCCCAGCT 180
Db 121 AGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCCATTGCCCCAGCT 180
Qy 181 ATCTGTCACTTCATCAAAAGGACAGTAGAAGAAAGAGAGCTTCCACCTCAAAATGCCATCAT 240
Db 181 ATCTGTCACTTCATCAAAAGGACAGTAGAAGAAAGAGAGCTTCCACCTCAAAATGCCATCAT 240
Qy 241 TGGGATTAAGGAAGGCTATCGTTCAAGATGCCTCTGCCACAGTGTCTCCAAAGATGGA 300
Db 241 TGGGATTAAGGAAGGCTATCGTTCAAGATGCCTCTGCCACAGTGTCTCCAAAGATGGA 300
Qy 301 CCCCCACCCAGGAGCATCGTGGAAAGAGAGAGCTTCCAAACAGCTCTTCAAAAGCAA 360
Db 301 CCCCCACCCAGGAGCATCGTGGAAAGAGAGAGCTTCCAAACAGCTCTTCAAAAGCAA 360
Qy 361 GTGGATTGATGTGATTCGAGTGAGACTTTTCAACAAAGGTAATATCGGGAACCTCTCTC 420
Db 361 GTGGATTGATGTGATTCGAGTGAGACTTTTCAACAAAGGTAATATCGGGAACCTCTCTC 420
Qy 421 GGATTCATTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAGAAAGGATGGC 480
Db 421 GGATTCATTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAGAAAGGATGGC 480
Qy 481 ACCTACAAATGCCATCATTCGGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGAC 540
Db 481 ACCTACAAATGCCATCATTCGGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGAC 540
Qy 541 AGTGGTCCCAAGATGACCCCCACCCACGAGGAGCATCGTGGAAAGAAAGAGCTTCCA 600
Db 541 AGTGGTCCCAAGATGACCCCCACCCACGAGGAGCATCGTGGAAAGAAAGAGCTTCCA 600
Qy 601 ACCAGCTCTCAAGCAAGTGGATTGATGATATCTCCACTGACGTAAGGGATGACGCA 660
Db 601 ACCAGCTCTCAAGCAAGTGGATTGATGATATCTCCACTGACGTAAGGGATGACGCA 660
Qy 661 CAATCCCACTATCTCTCGCAAGACCTTCTCTATATAAGGAAGTTCATTTTGGAG 720
Db 661 CAATCCCACTATCTCTCGCAAGACCTTCTCTATATAAGGAAGTTCATTTTGGAG 720
Qy 721 AGGACGCTGGATCC 736
Db 721 AGGACGCTGGATCC 736

RESULT 2
US-10-075-105C-3
; Sequence 3, Application US/10075105C
; Publication No. US20050188432A1
; GENERAL INFORMATION:
; APPLICANT: Li Zhijian T
; APPLICANT: Gray, Dennis J
; TITLE OF INVENTION: Bi-Directional Dual Promoter Complex with Enhanced Promoter Activity
; FILE REFERENCE: Transgene Expression in Eukaryotes
; CURRENT FILING DATE: 2002-02-13
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: CaMV 35S
; FEATURE:
; OTHER INFORMATION:

US-10-075-105C-3
Query Match 81.2%; Score 597.4; DB 22; Length 1360;
Best Local Similarity 99.8%; Pred. No. 2.2e-191;
Matches 598; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 109 AGAAGCTTCTGCAGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTC 168
Db 762 ATAAGCTTCTGCAGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTC 821
Qy 169 CATTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAGAAAGAGGTCACCTAC 228
Db 822 CATTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAGAAAGAGGTCACCTAC 881
Qy 229 AAATGCCATCATTCGGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGT 288
Db 882 AAATGCCATCATTCGGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGT 941
Qy 289 CCAAAAGATGGACCCACCCACGAGGAGCATCGTGGAAAGAAAGAGAGCTTCCAAACCA 348
Db 942 CCAAAAGATGGACCCACCCACGAGGAGCATCGTGGAAAGAAAGAGAGCTTCCAAACCA 1001
Qy 349 TCTTCAAAGCAAGTGGATTGATGTGATTCAGTGAGACTTTTCAACAAAGGTAATATCG 408
Db 1002 TCTTCAAAGCAAGTGGATTGATGTGATTCAGTGAGACTTTTCAACAAAGGTAATATCG 1061
Qy 409 GGAACCTCTCGGATTTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAA 468
Db 1062 GGAACCTCTCGGATTTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAA 1121
Qy 469 AAGGAAGTGGACCTTCAAAATGCCATCATTCGGATAAAGAAAGGCTATCGTTCAAGAT 528
Db 1122 AAGGAAGTGGACCTTCAAAATGCCATCATTCGGATAAAGAAAGGCTATCGTTCAAGAT 1181
Qy 529 GCCTCTCCGACAGTGGTCCCAAGATGGACCCCAAGAGGAGCATCGTGGAAAAA 588
Db 1182 GCCTCTCCGACAGTGGTCCCAAGATGGACCCCAAGAGGAGCATCGTGGAAAAA 1241
Qy 589 GAGAGCTTCCACACCGCTTCAAAAGCAAGTGGATTGATGATATCTCCACTGACGTA 648
Db 1242 GAAGAGCTTCCACACCGCTTCAAAAGCAAGTGGATTGATGATATCTCCACTGACGTA 1301
Qy 649 AGGGATGAGCGACAATCCCACTATCTTCCGAAGACCTTCTCTATATAAGGAAGTTC 707
Db 1302 AGGGATGAGCGACAATCCCACTATCTTCCGAAGACCTTCTCTATATAAGGAAGTTC 1360

RESULT 3
US-09-943-692-33
; Sequence 33, Application US/09943692
; Patent No. US20020152496A1
; GENERAL INFORMATION:
; APPLICANT: FISCHHOFF, DAVID A.
; APPLICANT: FUCHS, ROY L.
; APPLICANT: LAVRIK, PAUL B.
; APPLICANT: McPHERSON, SYLVIA A.
; APPLICANT: PERLAK, FREDERICK J.
; TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
; FILE REFERENCE: MOBT:195--1
; CURRENT APPLICATION NUMBER: US/09/943,692
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/027,998
; PRIOR FILING DATE: 1998-02-23
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 33
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Cauliflower Mosaic Viral Promoter (CaMV35S)
US-09-943-692-33

Query Match 75.3%; Score 554; DB 9; Length 661;
Best Local Similarity 94.5%; Pred. No. 8e-177;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTCAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 20 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 79
Qy 176 CAGCTATCTGCACTTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGCACCTACAAATGCC 235
Db 80 CAGCTATCTGCACTTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGCACCTACAAATGCC 139
Qy 236 ATCAATTCGATAAAGGAAAGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295
Db 140 ATCAATTCGATAAAGGAAAGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 199
Qy 296 ATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAGAGCTTCCCAACCACTCTTCAA 355
Db 200 ATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAGAGCTTCCCAACCACTCTTCAA 259
Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 260 AGCAAGTGGATTGATGTGATGTGCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 319
Qy 412 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAG 471
Db 320 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAAG 379
Qy 472 GAAGTGGCACTCAAAATGTCATTCGATTAAGGAAAGGAGCTATCGTTCAAGATGCC 531
Db 380 GAAGTGGCTCTCAAAATGTCATTCGATTAAGGAAAGGAGCTATCGTTCAAGATGCC 439
Qy 532 TCTGCCGACAGTGTGCCAAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 591
Db 440 TCTGCCGACAGTGTGCCAAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 499
Qy 592 GACGTTCCAAACCACTCTTCAAGCAAGTGAATGTGATGTGATATCTCCACTGACGTAAG 651
Db 500 GACGTTCCAAACCACTCTTCAAGCAAGTGAATGTGATGTGATATCTCCACTGACGTAAG 559
Qy 652 GATGACGACAAATCCCACTATCTCTCGCAAGACCTTCTCTATATAAGGAAATTCATTT 711
Db 560 GATGACGACAAATCCCACTATCTCTCGCAAGACCTTCTCTATATAAGGAAATTCATTT 619
Qy 712 CATTTGGAGGACACGCTG 731
Db 620 CATTTGGAGGACACGCTG 639

RESULT 4
US-10-213-791-29
; Sequence 29, Application US/10213791
; Publication No. US20030106096A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/10/213,791
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/441,340
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/108,763
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 2107
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; OTHER INFORMATION: cassette comprising plant operable promoter linked
; OTHER INFORMATION: to a leader, intron, a sequence encoding an AMPA

OTHER INFORMATION: acetyltransferase, and termination sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (26)..(590)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (615)..(685)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (699)..(1148)
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1149)..(1426)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1427)..(1858)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (1869)..(2102)
; US-10-213-791-29

Query Match 75.3%; Score 554; DB 15; Length 2107;
Best Local Similarity 94.5%; Pred. No. 1.4e-176;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTCAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 87
Qy 176 CAGCTATCTGCACTTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGCACCTACAAATGCC 235
Db 88 CAGCTATCTGCACTTTCATCAAAAGGAGATAGTGGAAAAAGGAGGTGGCTCTTCAAAATGCC 147
Qy 236 ATCAATTCGATAAAGGAAAGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295
Db 148 ATCAATTCGATAAAGGAAAGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 207
Qy 296 ATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACCACTCTTCAA 355
Db 208 ATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACCACTCTTCAA 267
Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 268 AGCAAGTGGATTGATGTGATGTGCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 327
Qy 412 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAG 471
Db 328 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAAG 387
Qy 472 GAAGTGGGACCTACAAATGCCATTCATTCGATAAAGGAAAGGCTATCGTTCAAGATGCC 531
Db 388 GAAGTGGCTCTTACAAATGCCATTCATTCGATAAAGGAAAGGCTATCGTTCAAGATGCC 447
Qy 532 TCTGCCGACAGTGTGCCAAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 591
Db 448 TCTGCCGACAGTGTGCCAAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 507
Qy 592 GACGTTCCAAACCACTCTTCAAGCAAGTGAATGTGATGTGATATCTCCACTGACGTAAG 651
Db 508 GACGTTCCAAACCACTCTTCAAGCAAGTGAATGTGATGTGATATCTCCACTGACGTAAG 567
Qy 652 GATGACGACAAATCCCACTATCTCTCGCAAGACCTTCTCTATATAAGGAAATTCATTT 711
Db 568 GATGACGACAAATCCCACTATCTCTCGCAAGACCTTCTCTATATAAGGAAATTCATTT 627
Qy 712 CATTTGGAGGACACGCTG 731
Db 628 CATTTGGAGGACACGCTG 647

RESULT 5
US-10-213-791-25
; Sequence 25, Application US/10213791

```
; Publication No. US20030106096A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/10/213,791
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/441,340
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/108,763
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 2122
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:expression
; OTHER INFORMATION: cassette comprising plant promoter linked to
; OTHER INFORMATION: sequence encoding AMPA acetyl transferase linked
; OTHER INFORMATION: to termination sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (6)..(620)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (645)..(715)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (729)..(1178)
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1179)..(1406)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1407)..(1838)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (1849)..(2082)
; US-10-213-791-25

Query Match 75.3%; Score 554; DB 15; Length 2122;
Best Local Similarity 94.5%; Pred. No. 1.4e-176;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGCAGTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 8 TCCGATGTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 67

Qy 176 CAGCTATCTGCTCACTTTCATCAAAAGGACAGTAGAAAAGGAGTGGCACCTACAAATGCC 235
Db 68 CAGCTATCTGCTCACTTTCATCAAAAGGACAGTAGAAAAGGAGTGGCTCTACAAATGCC 127

Qy 236 ATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGGTCCCAAAG 295
Db 128 ATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGGTCCCAAAG 187

Qy 296 ATGACCCCCCACCACGAGGAGCATCGTGGAAAAGAACGTTCCAAACCACTCTTCAA 355
Db 188 ATGACCCCCCACCACGAGGAGCATCGTGGAAAAGAACGTTCCAAACCACTCTTCAA 247

Qy 356 AGCAAGTGGATTGATGTGAT---TGCAGTGAGACTTTTCAACAAGGGTAATATCGGAA 411
Db 248 AGCAAGTGGATTGATGTGATGTGTCGCGATGTGAGACTTTTCAACAAGGGTAATATCGGAA 307

Qy 412 AACCTCTCGGATTCATTGCCAGCTATCTGTCACCTTCAATCAAAAGGACAGTAGAAAAG 471
Db 308 AACCTCTCGGATTCATTGCCAGCTATCTGTCACCTTATTTGTGAAGATAGTGGAAAAG 367

Qy 472 GAAGGTGGCACTTACAAATGCCATCATTTGGCATTAAGGAAAGGCTATCGTTCAAGATGCC 531
Db 368 GAAGGTGGCTCTTACAAATGCCATCATTTGGCATTAAGGAAAGGCTATCGTTGAAGATGCC 427

; Publication No. US20030106096A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/10/213,791
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/441,340
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/108,763
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 2122
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:monocot
; OTHER INFORMATION: expression cassette comprising plant operable
; OTHER INFORMATION: promoter linked to an intron, a sequence coding
; OTHER INFORMATION: for an AMPA acetyltransferase, and a termination
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (26)..(640)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (670)..(1473)
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1498)..(1725)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1726)..(2157)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (2172)..(2427)
; US-10-213-791-31

Query Match 75.3%; Score 554; DB 15; Length 2436;
Best Local Similarity 94.5%; Pred. No. 1.5e-176;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGCAGTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 87

Qy 176 CAGCTATCTGCTCACTTTCATCAAAAGGACAGTAGAAAAGGAGTGGCACCTACAAATGCC 235
Db 88 CAGCTATCTGCTCACTTTCATTTGTGAAGATAGTGGAAAAGGAGTGGCTCTCTCAAAATGCC 147

RESULT 6
US-10-213-791-31
; Sequence 31, Application US/10213791
; Publication No. US20030106096A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/10/213,791
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/441,340
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/108,763
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:monocot
; OTHER INFORMATION: expression cassette comprising plant operable
; OTHER INFORMATION: promoter linked to an intron, a sequence coding
; OTHER INFORMATION: for an AMPA acetyltransferase, and a termination
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (26)..(640)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (670)..(1473)
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1498)..(1725)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1726)..(2157)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (2172)..(2427)
; US-10-213-791-31

Query Match 75.3%; Score 554; DB 15; Length 2436;
Best Local Similarity 94.5%; Pred. No. 1.5e-176;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
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Qy 236 ATCATTCGATAAAGGAAAGCTATCTTCAAGATGCTCTGCGCAGAGTGTCCTCCAAAG 295
Db 148 ATCATTCGATAAAGGAAAGCCATCGTTGAAGATGCTCTGCGCAGAGTGTCCTCCAAAG 207
Qy 296 ATGACACCCACCCACGAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACACGCTTCAA 355
Db 208 ATGACACCCACCCACGAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACACGCTTCAA 267
Qy 356 AGCAAGTGGATTGATGTGAT----TGCACTGAGAGCTTTTCAACAAAGGTAATATCGGA 411
Db 268 AGCAAGTGGATTGATGTGATGTGCGATGTGAGACTTTTCAACAAAGGTAATATCGGA 327
Qy 412 AACCTCTCGGATTCATATGCGCCAGCTATCTGTCACTTCAATCAAAAGACAGTAGAAAAG 471
Db 328 AACCTCTCGGATTCATATGCGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 387
Qy 472 GAAGTGGCAGCTCAATATGCAATATGCGATTAAGAAAGAGCTATCGTTCAAGATGCC 531
Db 388 GAAGTGGCTCTCAAAATGCAATATGCGATTAAGAAAGAGCTATCGTTGAAGATGCC 447
Qy 532 TCTGCCGACAGTGGTCCAAAGATGGACCCACCCACGAGGAGCATCGTGGAAAAAGAA 591
Db 448 TCTGCCGACAGTGGTCCAAAGATGGACCCACCCACGAGGAGCATCGTGGAAAAAGAA 507
Qy 592 GACGTTCCAAACCGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 651
Db 508 GACGTTCCAAACCGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 567
Qy 652 GATGACGACAAATCCCACTATCTTCCGAAAGCCCTTCTCTATATAAGGAAGTTCATT 711
Db 568 GATGACGACAAATCCCACTATCTTCCGAAAGCCCTTCTCTATATAAGGAAGTTCATT 627
Qy 712 CATTTGGAGAGGACACGCTG 731
Db 628 CATTTGGAGAGGACACGCTG 647
```

RESULT 7

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US-10-232-665-23
; Sequence 23, Application US/10232665
; Publication No. US20030115630A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/10/232,665
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 3469
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (664)..(734)
; OTHER INFORMATION: L-Ta.hcbl
; FEATURE:
; NAME/KEY: intron
; LOCATION: (748)..(1238)
; OTHER INFORMATION: I-Os.Act1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1241)..(3199)
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; OTHER INFORMATION: Cry3Bb1 variant 11231mv2
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (3217)..(3450)
; OTHER INFORMATION: T-Ta.hsp17
; US-10-232-665-23
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Query Match 75.3%; Score 554; DB 15; Length 3469;

Best Local Similarity 94.5%; Pred. No. 1.9e-176;

Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

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Qy 116 TCTGCACTGAGACTTTTCAACAAAGGGTAATATATCGGAAACCTCTCGGATTCATTTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATATCGGAAACCTCTCTCGGATTCATTTGCC 87
Qy 176 CAGCTATCTCTCACTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGCACCTACAAATGCC 235
Db 88 CAGCTATCTCTCACTTTATTGTGAAGATAGTGGAAAAAGGAGGTGGCTCTCTACAAATGCC 147
Qy 236 ATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTGGTCCCAAAG 295
Db 148 ATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTGGTCCCAAAG 207
Qy 296 ATGACACCCACCCACGAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACACGCTTCAA 355
Db 208 ATGACACCCACCCACGAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACACGCTTCAA 267
Qy 356 AGCAAGTGGATTGATGTGAT----TGCACTGAGAGCTTTTCAACAAAGGTAATATCGGA 411
Db 268 AGCAAGTGGATTGATGTGATGTGCGATGTGAGACTTTTCAACAAAGGTAATATCGGA 327
Qy 412 AACCTCTCGGATTCATATGCGCCAGCTATCTGTCACTTCAATCAAAAGACAGTAGAAAAG 471
Db 328 AACCTCTCGGATTCATATGCGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 387
Qy 472 GAAGTGGCAGCTCAATATGCAATATGCGATTAAGAAAGAGCTATCGTTCAAGATGCC 531
Db 388 GAAGTGGCTCTCAAAATGCAATATGCGATTAAGAAAGAGCTATCGTTGAAGATGCC 447
Qy 532 TCTGCCGACAGTGGTCCAAAGATGGACCCACCCACGAGGAGCATCGTGGAAAAAGAA 591
Db 448 TCTGCCGACAGTGGTCCAAAGATGGACCCACCCACGAGGAGCATCGTGGAAAAAGAA 507
Qy 592 GACGTTCCAAACCGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 651
Db 508 GACGTTCCAAACCGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 567
Qy 652 GATGACGACAAATCCCACTATCTTCCGAAAGCCCTTCTCTATATAAGGAAGTTCATT 711
Db 568 GATGACGACAAATCCCACTATCTTCCGAAAGCCCTTCTCTATATAAGGAAGTTCATT 627
Qy 712 CATTTGGAGAGGACACGCTG 731
Db 628 CATTTGGAGAGGACACGCTG 647
```

RESULT 8

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US-10-232-665-15
; Sequence 15, Application US/10232665
; Publication No. US20030115630A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/10/232,665
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 3754
; TYPE: DNA
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: expression
OTHER INFORMATION: cassette

FEATURE:
NAME/KEY: promoter

LOCATION: (25)..(640)

OTHER INFORMATION: P-CaMV.35S

FEATURE:
NAME/KEY: intron

LOCATION: (669)..(1472)

OTHER INFORMATION: I-Zm.Hsp70

FEATURE:
NAME/KEY: CDS

LOCATION: (1490)..(3448)

OTHER INFORMATION: Cry3Bb1 variant v11231

FEATURE:
NAME/KEY: terminator

LOCATION: (3475)..(3730)

OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription

OTHER INFORMATION: termination and polyadenylation sequence

US-10-232-665-15

Query Match 75.3%; Score 554; DB 15; Length 3754;
Best Local Similarity 94.5%; Pred. No. 1.9e-176;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

QY	116	TCGTCAGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCGATTCCATTGCC	175
DB	28	TCCGATGTGAGCTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCGATTCCATTGCC	87
QY	176	CAGCTATCTGTCACCTTCATCAAAAGGACAGTAGAAAGGAGGTGGCACCTACAAATGCC	235
DB	88	CAGCTATCTGTCACCTTTATTGTGAAGATAGTGGAAAGGAGGTGGCTCTTACAAATGCC	147
QY	236	ATCATTCGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAAG	295
DB	148	ATCATTCGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAAG	207
QY	296	ATGGACCCCAACCCACAGAGAGCATCGTGGAAAGAAAGAGCTTCCAAACACGCTTTCAA	355
DB	208	ATGGACCCCAACCCACAGAGAGCATCGTGGAAAGAAAGAGCTTCCAAACACGCTTTCAA	267
QY	356	AGCAAGTGGATTGATGTGAT- ---TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGA	411
DB	268	AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGA	327
QY	412	AACCTCTCGGATTCATTCGCCAGCTATCTGTCACCTTCATCAAAAGGACAGTAGAAAG	471
DB	328	AACCTCTCGGATTCATTCGCCAGCTATCTGTCACCTTTATTGTGAAGATAGTGGAAAG	387
QY	472	GAAGTGGACCTACAAATGCCATCATTCGGATAAGGAAGGCTATCGTTCAAGATGCC	531
DB	388	GAAGTGGCTCCTACAAATGCCATCATTCGGATAAGGAAGGCTATCGTTCAAGATGCC	447
QY	532	TCGCGCACAGTGGTCCCAAGATGGACCCCAACCCACAGGAGCATCGTGGAAAGAA	591
DB	448	TCGCGCACAGTGGTCCCAAGATGGACCCCAACCCACAGGAGCATCGTGGAAAGAA	507
QY	592	GAGCTTCCAAACCAAGCTTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG	651
DB	508	GAGCTTCCAAACCAAGCTTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG	567
QY	652	GATGACGCACAAATCCCACTATCTTCGCAAGACCCCTTCTATATAAGGAAGTTCATTT	711
DB	568	GATGACGCACAAATCCCACTATCTTCGCAAGACCCCTTCTATATAAGGAAGTTCATTT	627
QY	712	CATTGGAGAGGACACGCTG 731	
DB	628	CATTGGAGAGGACACGCTG 647	

RESULT 9

US-10-198-478-16
Sequence 16, Application US/10198478
Publication No. US20030188336A1
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxin
FILE REFERENCE: 38-21 (13547) B
CURRENT APPLICATION NUMBER: US/10/198,478
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/186,002
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 8349
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: completely synthesized
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(8349)
OTHER INFORMATION:
US-10-198-478-16

Query Match 75.3%; Score 554; DB 16; Length 8349;
Best Local Similarity 94.5%; Pred. No. 2.9e-176;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

QY	116	TCGTCAGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCGATTCCATTGCC	175
DB	1807	TCCGATGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCGATTCCATTGCC	1866
QY	176	CAGCTATCTGTCACCTTCATCAAAAGGACAGTAGAAAGGAGGTGGCACCTACAAATGCC	235
DB	1867	CAGCTATCTGTCACCTTTATTGTGAAGATAGTGGAAAGGAGGTGGCTCTTACAAATGCC	1926
QY	236	ATCATTCGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAAG	295
DB	1927	ATCATTCGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAAG	1986
QY	296	ATGGACCCCAACCCACAGAGAGCATCGTGGAAAGAAAGAGCTTCCAAACACGCTTTCAA	355
DB	1987	ATGGACCCCAACCCACAGAGAGCATCGTGGAAAGAAAGAGCTTCCAAACACGCTTTCAA	2046
QY	356	AGCAAGTGGATTGATGTGAT- ---TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGA	411
DB	2047	AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGA	2106
QY	412	AACCTCTCGGATTCATTCGCCAGCTATCTGTCACCTTCATCAAAAGGACAGTAGAAAG	471
DB	2107	AACCTCTCGGATTCATTCGCCAGCTATCTGTCACCTTTATTGTGAAGATAGTGGAAAG	2166
QY	472	GAAGTGGCACCTTACAAATGCCATCATTCGGATAAAGGAAGGCTATCGTTCAAGATGCC	531
DB	2167	GAAGTGGCTCTTACAAATGCCATCATTCGGATAAAGGAAGGCTATCGTTGAAGATGCC	2226
QY	532	TCGCGCACAGTGGTCCCAAGATGGACCCCAACCCACAGGAGCATCGTGGAAAGAA	591
DB	2227	TCGCGCACAGTGGTCCCAAGATGGACCCCAACCCACAGGAGCATCGTGGAAAGAA	2286
QY	592	GAGCTTCCAAACCAAGCTTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG	651
DB	2287	GAGCTTCCAAACCAAGCTTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG	2346
QY	652	GATGACGCACAAATCCCACTATCTTCGCAAGACCCCTTCTATATAAGGAAGTTCATTT	711
DB	2347	GATGACGCACAAATCCCACTATCTTCGCAAGACCCCTTCTATATAAGGAAGTTCATTT	2406
QY	712	CATTGGAGAGGACACGCTG 731	
DB	2407	CATTGGAGAGGACACGCTG 2426	

RESULT 10

US-10-378-810-2/c
; Sequence 2, Application US/10378810
; Publication No. US20030213009A1
; GENERAL INFORMATION:
; APPLICANT: Ruben-Wilson, Beth
; APPLICANT: Smith, Kelley A
; TITLE OF INVENTION: PROMOTER AND INTRON FROM MAIZE ACTIN DEPOLYMERIZING
; TITLE OF INVENTION: FACTOR
; FILE REFERENCE: 58695
; CURRENT APPLICATION NUMBER: US/10/378,810
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/167,111
; PRIOR FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5796
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pDAB305
US-10-378-810-2

Query Match 74.9%; Score 551.4; DB 17; Length 5796;
Best Local Similarity 93.2%; Pred. No. 1.8e-175;
Matches 588; Conservative 0; Mismatches 41; Indels 2; Gaps 1;
Qy 105 CTGCAGAGCTTCCTGCAGTGAGACTTTTCAACAAGGGTAATATCGGGAAACCTCTCGG 164
Db 3550 CTGCAGATCTGCATGGGTGGAGACTTTTCAACAAGGGTAATATCGGGAAACCTCTCGG 3491
Qy 165 ATTCATGCCCCAGCTATCTGTCTCTCATCAAAAGGACAGTACAAAAGGAGTGGCAC 224
Db 3490 ATTCATGCCCCAGCTATCTGTCTCTCATTTTGTGAAGATAGTGGAAAAGGAGTGGCTC 3431
Qy 225 CTACAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAG 284
Db 3430 CTACAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTGAAGATGCTCTGCCGACAG 3371
Qy 285 TGGTCCAAAGATGGAGCCCCCACCACGAGAGGATCGTGGAAAAGGAAAGACGTTCCAAC 344
Db 3370 TGGTCCAAAGATGGAGCCCCCACCACGAGAGGATCGTGGAAAAGGAAAGACGTTCCAAC 3311
Qy 345 CACGTCTTCAAGCAAGTGGATTGATGTGAT--TGCAGTGGAGCTTTTCAACAAGGTA 402
Db 3310 CACGTCTTCAAGCAAGTGGATTGATGTGATCATCGATGGAGACTTTTCAACAAGGTA 3251
Qy 403 ATATCGGAAACCTCTCGGATTCATTGCCAGCTATCTGTCACTTCAATCAAAAGGACA 462
Db 3250 ATATCGGAAACCTCTCGGATTCATTGCCAGCTATCTGTCACTTATTTGTGAAGATA 3191
Qy 463 GTAGAAAAGGAGGTGGCACCCTACAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTT 522
Db 3190 GTGAAAAGGAGGTGGCTCTCTACAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTT 3131
Qy 523 CAAGATGCTCTGCCGACAGTGGTCCCAAGATGGAGCCCCCACCACGAGAGGATCGTG 582
Db 3130 GAAGATGCTCTGCCGACAGTGGTCCCAAGATGGAGCCCCCACCACGAGAGGATCGTG 3071
Qy 583 GAAAAGGAGAGCTTTCAACACCACTCTTCAAGCAAGTGGATTGATGTGATCTCCACT 642
Db 3070 GAAAAGGAGAGCTTTCCACCACGCTCTTCAAGCAAGTGGATTGATGTGATCTCCACT 3011
Qy 643 GACGTAAAGGATGACGCAAAATCCCACTATCTTTGCAAGACCCCTTCTCTATATAAGGA 702
Db 3010 GACGTAAAGGATGACGCAAAATCCCACTATCTTTGCAAGACCCCTTCTCTATATAAGGA 2951
Qy 703 AGTTCATTTCAATTTGGAGAGGACAGCTGGA 733
Db 2950 AGTTCATTTCAATTTGGAGAGAACACGGGGGA 2920

RESULT 11

US-10-759-602-26
; Sequence 26, Application US/10759602
; Publication No. US20040143868A1
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; APPLICANT: Armstrong, Katherine
; Belmar, Scott
; Folkerts, Otto
; Hopkins, Nicole
; Menke, Michael A.
; Paredy, Dayakar
; Petolino, Joseph F.
; Smith, Kelley
; Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DowAgroSciences LLC
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/759,602
; FILING DATE: 16-Jan-2004
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 5110
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5897 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-759-602-26

Query Match 74.9%; Score 551.4; DB 19; Length 5897;
Best Local Similarity 93.2%; Pred. No. 1.9e-175;
Matches 588; Conservative 0; Mismatches 41; Indels 2; Gaps 1;
Qy 105 CTGCAGAGCTTCCTGCAGTGAGACTTTTCAACAAGGGTAATATCGGGAAACCTCTCGG 164
Db 12 CTGCAGATCTGCATGGGTGGAGACTTTTCAACAAGGGTAATATCGGGAAACCTCTCGG 71
Qy 165 ATTCCATTGCCAGCTATCTGTCTCATCAAAAGGACAGTACAAAAGGAGTGGCAC 224
Db 72 ATTCCATTGCCAGCTATCTGTCTCATTTATTTGTGAAGATAGTGGAAAAGGAGTGGCTC 131
Qy 225 CTACAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAG 284
Db 132 CTACAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTGAAGATGCTCTGCCGACAG 191
Qy 285 TGGTCCAAAGATGGAGCCCCCACCACGAGAGGATCGTGGAAAAGGAAAGACGTTCCAAC 344
Db 192 TGGTCCAAAGATGGAGCCCCCACCACGAGAGGATCGTGGAAAAGGAAAGACGTTCCAAC 251
Qy 345 CACGTCTTCAAGCAAGTGGATTGATGTGAT--TGCAGTGGAGCTTTTCAACAAGGTA 402
Db 252 CACGTCTTCAAGCAAGTGGATTGATGTGATCATCGATGGAGACTTTTCAACAAGGTA 311

QY 403 ATATCGGAAACCTCTCGGATTCATTGCCAGCTATCTGTCACTTCATCAAAAGGACA 462
| | | | |
Db 312 ATATCCGGAACCTCTCGGATTCATTGCCAGCTATCTGTCACTTCATGGAAGATA 371
| | | | |
QY 463 GTAGAAAAGGAAGTGCACCTACAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTT 522
| | | | |
Db 372 GTGAAAAGGAAGTGGCTCTCTACAAATGCCATCATTTGCGATAAAGGAAAGGCCATCGTT 431
| | | | |
QY 523 CAGATCGCTCTGCGGACAGTGGTCCCAAAGATGGACCCCAACCCACGAGGAGCATCGTG 582
| | | | |
Db 432 GAAGATCGCTCTGCGGACAGTGGTCCCAAAGATGGACCCCAACCCACGAGGAGCATCGTG 491
| | | | |
QY 583 GAAAAGAAGACGTTTCCAAACCACTCTTTCAAAGCAAGTGGATTGATGTGATATCTCCACT 642
| | | | |
Db 492 GAAAAGAAGACGTTTCCAAACCACTCTTTCAAAGCAAGTGGATTGATGTGATATCTCCACT 551
| | | | |
QY 643 GAGTAAGGATGACGACCAATCCCACTATCTTTGCAAGACCTTCCCTCTATATAAGGA 702
| | | | |
Db 552 GAGTAAGGATGACGACCAATCCCACTATCTTTGCAAGACCTTCCCTCTATATAAGGA 611
| | | | |
QY 703 AGTTCATTTCATTGGAGAGGACACGCTGGA 733
| | | | |
Db 612 AGTTCATTTCATTGGAGAGGACACGCTGGA 642
| | | | |

RESULT 12
US-10-759-602-19
; Sequence 19, Application US/10759602
; Publication No. US20040143868A1
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; Armstrong, Katherine
; Belmar, Scott
; Folkerts, Otto
; Hopkins, Nicole
; Menke, Michael A.
; Paredy, Davakar
; Petolino, Joseph P.
; Smith, Kelley
; Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DowAgroSciences LLC
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING APPLICATION NUMBER: US/10/759,602
; FILING DATE: 16-Jan-2004
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 5110
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-759-602-19

Query Match 74.8%; Score 550.4; DB 19; Length 9335;
Best Local Similarity 93.2%; Pred. No. 5.1e-175;
Matches 587; Conservative 0; Mismatches 41; Indels 2; Gaps 1;
QY 106 TGCAGAAAGCTTCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTTCCTCGGA 165
| | | | |
Db 4852 TGCAGATTCGATGGGTGGAGACTTTTCAACAAAGGGTAATATCCGGAACCTTCCTCGGA 4911
| | | | |
QY 166 TTCCATTTGCCAGCTATCTGTCTACTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCACC 225
| | | | |
Db 4912 TTCCATTTGCCAGCTATCTGTCTACTTTATTTGTGAAGATAGTGAAAAGGAGGTGGCTCC 4971
| | | | |
QY 226 TCAAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATCCCTCTGCGGACAGT 285
| | | | |
Db 4972 TCAAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTGAAGATGCCCTCTGCCGACAGT 5031
| | | | |
QY 286 GGTCCCAAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAGAAAGACGTTTCCAACC 345
| | | | |
Db 5032 GGTCCCAAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAGAAAGACGTTTCCAACC 5091
| | | | |
QY 346 ACCTCTTCAAAGCAAGTGGATTGATGTGAT--TGCAGTGAGACTTTTCAACAAAGGGTAA 403
| | | | |
Db 5092 ACCTCTTCAAAGCAAGTGGATTGATGTGATCATCGATGGAGACTTTTCAACAAAGGGTAA 5151
| | | | |
QY 404 TATCGGGAAACCTCTCGGATTCCTATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAG 463
| | | | |
Db 5152 TATCGGGAAACCTCTCGGATTCCTATTCGCCAGCTATCTGTCACTTTATTTGGAAGATAG 5211
| | | | |
QY 464 TAGAAAAGGAAGTGGCGACCTTCAAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTC 523
| | | | |
Db 5212 TGGAAAAGGAAGTGGCTCTCTACAAATGCCATCATTTGCGATAAAGGAAAGGCCATCGTTG 5271
| | | | |
QY 524 AGATGCCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCAACCCACGAGGAGCATCGTGG 583
| | | | |
Db 5272 AGATGCCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCAACCCACGAGGAGCATCGTGG 5331
| | | | |
QY 584 AAAAAAGAACGTTTCCAAACCACTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTG 643
| | | | |
Db 5332 AAAAAAGAACGTTTCCAAACCACTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTG 5391
| | | | |
QY 644 ACCTAAGGATGACGACCAATCCCACTATCTTTGCAAGACCTTCCCTCTATATAAGGAA 703
| | | | |
Db 5392 ACCTAAGGATGACGACCAATCCCACTATCTTTGCAAGACCTTCCCTCTATATAAGGAA 5451
| | | | |
QY 704 GTTCATTTTCATTGGAGAGGACACGCTGGA 733
| | | | |
Db 5452 GTTCATTTTCATTGGAGAGGACACGCTGGA 5481
| | | | |

RESULT 13
US-10-198-478-14
; Sequence 14, Application US/10198478
; Publication No. US20030188336A1
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxin
; FILE REFERENCE: 38-21 (13547) B
; CURRENT APPLICATION NUMBER: US/10/198,478
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/186, 002
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 10249
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: (1)..(10249)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3597)..(3670)
; OTHER INFORMATION: "n" = g, a, c, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4292)..(4344)
; OTHER INFORMATION: "n" = g, a, c, or t
US-10-198-478-14

Query Match      74.7%; Score 550; DB 16; Length 10249;
Best Local Similarity 94.5%; Pred. No. 7.3e-175;
Matches 582; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 19 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 78
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 139 ATCATTCGGATAAAGGAGGCTATCGTTGAAGATGCTCTGCCGACAGTGGTCCCAAAG 198
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Qy 296 ATGACACCCACCCACGAGGAGCATCGTGGAAAGAGAGCTTCCAAACACGCTCTTCAA 355
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 199 ATGACACCCACCCACGAGGAGCATCGTGGAAAGAGAGCTTCCAAACACGCTCTTCAA 258
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 499 GACGTTCCAAACCGCTCTTCAAGCAAGTGGAATTGATGTGATATCTCCACTGACGTAAG 558
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 652 GATCAGCACAATCCCACTATCTTCGCAAGACCTTCTCTATATAAGGAAGTTCAATT 711
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 559 GATCAGCACAATCCCACTATCTTCGCAAGACCTTCTCTATATAAGGAAGTTCAATT 618
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 14
US-10-198-478-15
; Sequence 15, Application US/10198478
; Publication No. US20030188336A1
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotox
; FILE REFERENCE: 38-21 (13547) B
; CURRENT APPLICATION NUMBER: US/10/198,478
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/186, 002
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RESULT 15

US-10-198-478-13
; Sequence 13, Application US/10198478
; Publication No. US2003018836A1
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotox
; FILE REFERENCE: 38-21 (13547) B
; CURRENT APPLICATION NUMBER: US/10/198,478
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 05/186, 002
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 10339
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; ORGANISM: artificial sequence
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; LOCATION: (4382)..(4434)
; OTHER INFORMATION: "n" = g, a, c, or t
US-10-198-478-13

Query Match 74.7%; Score 550; DB 16; Length 10339;
Best Local Similarity 94.5%; Pred. No. 7.3e-175;
Matches 582; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
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QY 176 CAGCTATCTGCTCATCAAAAGGACGTAGAAAAGGAGGTGGCACCTACAAATGCC 235
DB 79 CAGCTATCTGCTCATTTATTTGTAAGATAGTGAAGAGGAGGTGGCTCTCAAAATGCC 138
QY 236 ATCATTCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295
DB 139 ATCATTCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 198
QY 296 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGAGACGTTCNAACACGCTTTCAA 355
DB 199 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGAGACGTTCNAACACGCTTTCAA 258
QY 356 AGCAAGTGGATTGATGTGAT---TGCAGTGAGACTTTTCAACAAGGGTAATATCGGGA 411
DB 259 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAGGGTAATATCGGGA 318
QY 412 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
DB 319 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTTGTGGAAGATAGTGGAAAAG 378
QY 472 GAAGGTGGACCTACAAATGCCATCATTTGGGATAAAGGAAGGCTATCGTTCAAGATGCC 531
DB 379 GAAGGTGGCTCCTACAAATGCCATCATTTGGGATAAAGGAAGGCTATCGTTGAAGATGCC 438
QY 532 TCTGCCGACAGTGGTCCCAAGATGGACCCACCCACGAGGAGCATCGTGGAAAAGAA 591
DB 439 TCTGCCGACAGTGGTCCCAAGATGGACCCACCCACGAGGAGCATCGTGGAAAAGAA 498
QY 592 GACGTTCCAAACCGCTTTCAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 651
DB 499 GACGTTCCAAACCGCTTTCAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 558

QY 652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCTCTATATAAGGAAGTTCATTT 711
DB 559 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCTCTATATAAGGAAGTTCATTT 618
QY 712 CATTTGGAGAGGACAC 727
DB 619 CATTTGGAGAGGACAC 634

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 14:58:28 ; Search time 3213 Seconds
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Title: US-10-075-105C-1

Perfect score: 736

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Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	546.6	74.3	698	7	CK438483
2	546.6	74.3	702	7	C0472768
3	546.6	74.3	755	7	CK438332
4	546.6	74.3	803	7	C0472761
5	544.6	74.0	713	7	CK437984
6	544.6	74.0	741	7	CK438362
7	537.2	73.0	655	7	CK437920
8	535.2	72.7	736	7	CK438485
9	533.2	72.4	698	7	CK438348
10	480.8	65.3	610	7	C0481168
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c	30	332.6	45.2	574	8	BH913058
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c	39	332.6	45.2	586	9	CG805042
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c	42	332.6	45.2	609	8	BH913533
c	43	332.6	45.2	614	9	CG709523
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ALIGNMENTS

RESULT 1
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LOCUS CK438483 698 bp mRNA linear EST 08-JAN-2004
DEFINITION GQ0085.BR_M18 GQ008: Cambium, phloem and bark of girdled saplings
Picea glauca cDNA clone GQ0085_M18 5', mRNA sequence.
ACCESSION CK438483
VERSION CK438483.1 GI:40769778
KEYWORDS EST.
SOURCE Picea glauca (white spruce)
ORGANISM Picea glauca
REFERENCE 1 (bases 1 to 698)
AUTHORS Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A., Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J., Siddiqui,A., Holt,R., Marra,M. and Mackay,J.
Arborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)
CONTACT: John Mackay
Centre de Recherche en Biologie Forestiere
Universite Laval
Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
Fax: 418 656 7493

Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MN5174605 Clone ID:
GQ0085 M18 Clones available through: John Mackay, Ph. D. Professeur
adjoint -Assistant professeur EMAIL: jmackay@rsvs.ulaval.ca Centre
de Recherche en Biologie Forestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
Plate: 5 row: 18 column: M
Seq primer: M13 Reverse Primer.

FEATURES

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/mol_type="mRNA"
/strain="pg-653"
/db_xref="taxon:3330"
/clone="GQ0085_M18"
/sex="Hermaphrodite"
/tissue_type="Vascular cambium, secondary phloem and bark
of trees girdled by removing a ring of bark ca. 1 cm wide
from the midpoint of the main stem"
/dev_stage="Vascular cambium, secondary phloem, and bark
from trees harvested 1 and 7 days after girdling
treatment"
/lab_host="E. coli DH10B cells"


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478 GGCACTTACAAATGCCATCATTTGGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCC 537
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598 CCAACCACTCTTCAAGCAAGTGGATGATGCTGATATCTCCATGACGTGAAGGATGAC 657
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RESULT 3
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LOCUS
DEFINITION
GQ0083_BR_H02 GQ008: Cambium, phloem and bark of girdled saplings
Picea glauca cDNA clone GQ0083_H02 5', mRNA sequence.
ACCESSION
CK438332
VERSION
CK438332.1 GI:40769292
KEYWORDS
EST.
SOURCE
Picea glauca (white spruce)
ORGANISM
Picea glauca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
1 (bases 1 to 755)
Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
Siddiqui A., Holt,R., Marra,M. and Mackay,J.
Aborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)
Contact: John Mackay
Centre de Recherche en Biologie Forestiere
Universite Laval
Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
Fax: 418 656 7493
Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MN5173701 Clone ID:
GQ0083_H02 Clones available through: John Mackay, Ph. D. Professeur
adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
de Recherche en Biologie Forestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
Plate: 3 row: 02 column: H
Seq primer: M13 Reverse Primer.
Location/Qualifiers
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/organism="Picea glauca"
/mol_type="mRNA"
/strain="pg-653"
/db_xref="taxon:3330"
/clone="GQ0083_H02"
/sex="Hermaphrodite"
/tissue_type="Vascular cambium, secondary phloem and bark
of trees girdled by removing a ring of bark ca. 1 cm wide
from the midpoint of the main stem"
/dev_stage="Vascular cambium, secondary phloem, and bark
from trees harvested 1 and 7 days after girdling
treatment"
/lab_host="E. coli DH10B cells"
/clone_lib="GQ008: Cambium, phloem and bark of girdled
saplings"

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FEATURES

source

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RESULT 4
CO472761
LOCUS
DEFINITION
GQ0081_BR_1.G07 GQ008: Cambium, phloem and bark of girdled saplings
Picea glauca cDNA clone GQ0081_BR_G07 5', mRNA sequence.
ACCESSION
CO472761
VERSION
CO472761.1 GI:50141306
KEYWORDS
EST.
SOURCE
Picea glauca (white spruce)
ORGANISM
Picea glauca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
1 (bases 1 to 803)
Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,

```

/note="Organ: Main stem of 4 year old saplings, approximately 60 cm tall; Vector: pBluescript II SK (+) XR; Site 1: Eco-RI; Site 2: Xho-I; Tissues were pooled from above and below the girdle. cDNA was prepared from 5 mg of poly A+ selected RNA and was directionally ligated into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH10B cells (in vitrogen) for propagation"

ORIGIN

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Query Match      74.3%; Score 546.6; DB 7; Length 755;
Best Local Similarity 94.7%; Pred. No. 1.9e-160;
Matches 577; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

Qy 121 AGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCCGATTCCATTGCGCCAGCT 180
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Db 32 ATTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCCGATTCCATTGCGCCAGCT 91
    |||||
Qy 181 ATCTGTCACTTCATCAAAAGGACAGTAGATAAAAGGAAGGTGGCACCTTCAAAATGCCATCAT 240
    |||||
Db 92 ATCTGTCACTTTATTGTGAAGATAGTGAAGGAAGGTGGCTCTCTACAAATGCCATCAT 151
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Qy 241 TCGGATAAAGGAAAGGCTATCGTTCAAGATCCCTCTCGGACAGTGGTCCCAAGATGGA 300
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Db 152 TCGGATAAAGGAAAGGCGCATCGTTGAAGATGCCCTCTCGGACAGTGGTCCCAAGATGGA 211
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Qy 301 CCCCACCCACGAGGAGCATCGTGGAAAGGAAGAGACGTTCACACACAGCTCTTCAAAGCAA 360
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Db 452 GACAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAGGAAGAGCTT 511
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Db 512 CCAACCACTCTTCAAGCAAGTGGATGATGATATCTCCATGACGTGAAGGATGAC 571
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Qy 658 GCACAATCCCACTATCTTCCGAAAGACCTTCCCTCTATATAAGGAAGTTCATTTTCATTG 717
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Db 572 GCACAATCCCACTATCTTCCGAAAGACCTTCCCTCTATATAAGGAAGTTCATTTTCATTG 631
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Qy 718 GAGAGGACA 726
    |||||
Db 632 GAGAGGAGA 640

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XR; Site_1: Eco-RI; Site_2: Xho-I; Tissues were pooled from above and below the girdle. cDNA was prepared from 5 mg of poly A+ selected RNA and was directionally ligated into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH10B cells (in vitrogen) for propagation"

ORIGIN

```
Query Match          74.0%; Score 544.6; DB 7; Length 713;
Best Local Similarity 94.4%; Pred. No. 7.9e-160;
Matches 575; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

Qy 121 AGTGAGACTTTTCAACAAAGGGTAATATCGGGAACCTCTCGGATTCATTCGCCAGCT 180
Db 4 ATTGAGACTTTTCAACAAAGGGTAATATCGGGAACCTCTCGGATTCATTCGCCAGCT 63

Qy 181 ATCTGTCACTTCATCAAAAGGACAGTAGAAGAGGTGCGACCTCAAAATGCCATCAT 240
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Qy 538 GACAGTGTGTCCTCAAGATGAGACCCACCCAGGAGGAGCATCGTGGAAAAGAGAGCGTT 597
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Qy 658 GCACAAATCCCACTATCCTTGCAGAGACCTTCTCTATATAAGGAAGTTCATTTCAATTG 717
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Qy 718 GAGAGGACA 726
Db 604 GAGAGGAGA 612
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RESULT 6

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CK438362
LOCUS CK438362
DEFINITION GQ0083.BR J24 GQ008: Cambium, phloem and bark of girdled saplings
Picea glauca cDNA clone GQ0083_J24 5', mRNA sequence.
CK438362
ACCESSION CK438362.1 GI:40769522
VERSION 1
KEYWORDS EST.
SOURCE Picea glauca (white spruce)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE 1 (bases 1 to 741)
AUTHORS Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A.,
Retzel, E., Butterfield, Y., Barber, S., Fang, G., Scott, J.,
Siddiqui, A., Holt, R., Marra, M. and Mackay, J.
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TITLE
JOURNAL
COMMENT

Arborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)
Contact: John Mackay
Centre de Recherche en Biologie Forestiere
Universite Laval
Pavillon Charles-Eugene Marchand, Quebec, Canada G1K 7P4
Fax: 418 656 7493
Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MN5173771 Clone ID:
GQ0083_J24 Clones available through: John Mackay, Ph. D. Professeur
adjoint - Assistant professeur EMAIL: jmackay@rsvs.ulaval.ca Centre
de Recherche en Biologie Forestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
Plate: 3 row: 24 column: J
Seq primer: M13 Reverse Primer.

FEATURES

source

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1. 741
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/mol_type="mRNA"
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/db_xref="taxon:3330"
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/tissue_type="Vascular cambium, secondary phloem and bark
of trees girdled by removing a ring of bark ca. 1 cm wide
from the midpoint of the main stem"
/dev_stage="Vascular cambium, secondary phloem, and bark
from trees harvested 1 and 7 days after girdling
treatment"
/lab_host="E. coli DH10B cells"
/clone_lib="GQ008: Cambium, phloem and bark of girdled
saplings"
/notes="Organ: Main stem of 4 year old saplings
approximately 60 cm tall; Vector: pBluescript II SK (+)
XR; Site_1: Eco-RI; Site_2: Xho-I; Tissues were pooled
from above and below the girdle. cDNA was prepared from 5
mg of poly A+ selected RNA and was directionally ligated
into the pBluescript II SK (+) XR vector (Stratagene),
transformed by electroporation into DH10B cells (in
vitrogen) for propagation"
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ORIGIN

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Query Match          74.0%; Score 544.6; DB 7; Length 741;
Best Local Similarity 94.4%; Pred. No. 7.9e-160;
Matches 575; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

Qy 121 AGTGAGACTTTTCAACAAAGGGTAATATCGGGAACCTCTCGGATTCATTCGCCAGCT 180
Db 37 ATTGAGACTTTTCAACAAAGGGTAATATCGGGAACCTCTCGGATTCATTCGCCAGCT 96

Qy 181 ATCTGTCACTTCATCAAAAGGACAGTAGAAGAGGTGCGACCTCAAAATGCCATCAT 240
Db 97 ATCTGTCACTTTATTTGGAAGATAGTGGAAGAGGAGGTGGCTCTCAAAATGCCATCAT 156

Qy 241 TCGGATAAAGAAAGGGTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAGATGGA 300
Db 157 TCGGATAAAGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAGATGGA 216

Qy 301 CCCCCACCCAGGAGGAGCATCGTGGAAAAGAGAGAGCTTCCAAACAGCTCTTCAAAGCAA 360
Db 217 CCCCCACCCAGGAGGAGCATCGTGGAAAAGAGAGAGCTTCCAAACAGCTCTTCAAAGCAA 276

Qy 361 GTGGATTGATGTGATTG---CAGTGAGACTTTTCAACAAAGGGTAATATCGGGAACCTC 417
Db 277 GTGGATTGATGTGATTGCGGATTTGAGACTTTTCAACAAAGGGTAATATCGGGAACCTC 336

Qy 418 CTCGGATTCCATTCGCCAGCTATCTGTCACTTCAAAAGGACAGTAGAAAAGGAAGGT 477
Db 337 CTCGGATTCCATTCGCCAGCTATCTGTCACTTTATTTGGAAGATAGTGGAAGAGAGGT 396

Qy 478 GGCACCTTCAAAATGCCATCATTCGATAAAGGAAGGCTATCGTTCAAGATGCTCTTGCC 537
Db 478 GGCACCTTCAAAATGCCATCATTCGATAAAGGAAGGCTATCGTTCAAGATGCTCTTGCC 537
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Db 397 GGCTCTACAAATGCCATCATTCGATATAAGGAAAGGCCATCGTTGAAGATGCTCTGCG 456

Qy 538 GACAGTGGTCCCAAGATGACCCACCCACGAGGAGCATCGTGAAAAGAGACGTT 597

Db 457 GACAGTGGTCCCAAGATGACCCACCCACGAGGAGCATCGTGAAAAGAGACGTT 516

Qy 598 CCAACACAGCTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGAC 657

Db 517 CCAACACAGCTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGAC 576

Qy 658 GCACAAATCCCACTATCTTCGCAAGACCTTCCTCTATATAAGAAAGTTCATTTCATTG 717

Db 577 GCACAAATCCCACTATCTTCGCAAGACCTTCCTCTATATAAGAAAGTTCATTTCATTG 636

Qy 718 GAGAGGACA 726

Db 637 GAGAGGAGA 645

RESULT 7

CK437920

LOCUS

DEFINITION

Q00081_BR_F05 Q0008: Cambium, phloem and bark of girdled saplings

Picea glauca cDNA clone Q00081_F05 5', mRNA sequence.

CK437920

CK437920.1 GI:40768406

EST.

SOURCE

Picea glauca (white spruce)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

REFERENCE

AUTHORS

Morency M.-J., Cooke J., Pavy N., Parsons L., Paule C., Seguin A., Retzel E., Butterfield Y., Barber S., Yang G., Stott J., Siddiqui A., Holt R., Marra M. and Mackay J.

Arborea EST sequencing in Picea glauca (white spruce)

Unpublished (2004)

Contact: John Mackay

Centre de Recherche en Biologie Forestiere

Universite Laval

Pavillon Charles-Eugene Marchand, Quebec, Canada G1K 7P4

Fax: 418 656 7493

Email: jmackay@svs.ulaval.ca

Center for Computational Genomics and Bioinformatics (CCGB), University of Minnesota, MN id Identifier: MN5171736 Clone ID: Q00081_F05 Clones available through: John Mackay, Ph. D. Professeur adjoint - Assistant professor EMAIL: jmackay@svs.ulaval.ca Centre de Recherche en Biologie Forestiere (Forest Biology Research Center) Universite Laval Quebec, Quebec CANADA G1K 7P4

Plate: 1 row: 05 column: F

Seq primer: M13 Reverse Primer.

FEATURES

source

1. .655

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/mol_type="mRNA"

/strain="pg-653"

/db_xref="taxon:3330"

/clone="Q00081_F05"

/sex="Hermaphrodite"

/tissue_type="Vascular cambium, secondary phloem and bark of trees girdled by removing a ring of bark ca. 1 cm wide from the midpoint of the main stem"

/dev_stage="Vascular cambium, secondary phloem, and bark from trees harvested 1 and 7 days after girdling treatment"

/lab_host="E. coli DH10B cells"

/clone_lib="Q0008: Cambium, phloem and bark of girdled saplings"

/notes="Organ: Main stem of 4 year old saplings, approximately 60 cm tall; Vector: pBluescript II SK (+) XR; Site1: EcoRI; Site2: Xho-I; Tissues were pooled from above and below the girdle. cDNA was prepared from 5 mg of poly A+ selected RNA and was directionally ligated

ORIGIN

Query Match 73.0%; Score 537.2; DB 7; Length 655;

Best Local Similarity 92.5%; Pred. No. 1.6e-157;

Matches 567; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Qy 121 AGTGAGACTTTTCAACAAAGGGTAAATATCGGAAACCTCTCGGATTCATTGCCAGCT 180

Db 24 ATTGAGACTTTTCAACAAAGGGTAAATATCGGAAACCTCTCGGATTCATTGCCAGCT 83

Qy 181 ATCTGTCACCTTCATCAAAAGGACAGTAGAAAAGAGGTGGCACCTACAAAATGCCATCAT 240

Db 84 ATCTGTCACCTTTATTGTGAAGATAGTGGAAAAGAGAGGTGGCTCTTACAAAATGCCATCAT 143

Qy 241 TCGATATAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAGATGGA 300

Db 144 TCGATATAAGGAAAGGCTATCGTTGAAGATGCTCTGCCGACAGTGGTCCCAAGATGGA 203

Qy 301 CCCCACCCACGAGGAGCATCGTGAAAAGAGAGCTTCCACACAGCTCTTCAAAAGCAA 360

Db 204 CCCCACCCACGAGGAGCATCGTGAAAAGAGAGCTTCCACACAGCTCTTCAAAAGCAA 263

Qy 361 GTGGATTGATGTGATTG---CAGTGAAGCTTTTCAACAAAGGTAATATCGGAAAACCTC 417

Db 264 GTGGATTGATGTGATGTCGATTGAGACTTTTCAACAAAGGTAATATCGGAAAACCTC 323

Qy 418 CTCGGATTCATTGCCAGCTATCTGTCTACTTCATCAAAAGGACAGTAGAAAAGGAAGGT 477

Db 324 CTCGGATTCATTGCCAGCTATCTGTCTACTTTATTGTGAAGATAGTGGAAAAGGAAGGT 383

Qy 478 GGCACCTACAAATGCCATCATTCGCGATAAGGAAAGGCTATCGTTCAAGATGCTCTGCC 537

Db 384 GGCTCTCAAAATGCCATCATTCGCGATAAGGAAAGGCTATCGTTCAAGATGCTCTGCC 443

Qy 538 GACAGTGGTCCCAAGATGGACCCCAACGAGGAGCATCGTGAAAAGGAAGACGTT 597

Db 444 GACAGTGGTCCCAAGATGGACCCCAACGAGGAGCATCGTGAAAAGGAAGACGTT 503

Qy 598 CCAACACAGCTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGAC 657

Db 504 CCAACACAGCTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGAC 563

Qy 658 GCACATCCCACTATCTTCGCAAGACCTTCCTCTATATAAGAAAGTTCATTTCATTG 717

Db 564 GCACATCCCACTATCTTCGCAAGACCTTCCTCTATATAAGAAAGTTCATTTCATTG 623

Qy 718 GAGAGGACACGCT 730

Db 624 GAGANNNNNNNT 636

RESULT 8

CK438485

LOCUS

DEFINITION

Q00085_BR_M24 Q0008: Cambium, phloem and bark of girdled saplings

Picea glauca cDNA clone Q00085_M24 5', mRNA sequence.

CK438485

CK438485.1 GI:40769782

EST.

SOURCE

Picea glauca (white spruce)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

REFERENCE

AUTHORS

Morency M.-J., Cooke J., Pavy N., Parsons L., Paule C., Seguin A., Retzel E., Butterfield Y., Barber S., Yang G., Stott J., Siddiqui A., Holt R., Marra M. and Mackay J.

Arborea EST sequencing in Picea glauca (white spruce)

Unpublished (2004)

Contact: John Mackay

into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH10B cells (in vitrogen) for propagation"

Centre de Recherche en Biologie Forestiere
 Universite Laval
 Pavillon Charles-Eugene Marchand, Quebec, Canada G1K 7P4
 Fax: 418 656 7493
 Email: jmackay@rsvs.ulaval.ca
 Center for Computational Genomics and Bioinformatics (CCGB),
 University of Minnesota, MN id Identifier: MN5174611 Clone ID:
 GQ0085 M24 Clones available through: John Mackay, Ph. D. Professeur
 adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
 de Recherche en Biologie Forestiere (Forest Biology Research
 Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
 Plate: 5 row: 24 column: M
 Seq primer: M13 Reverse Primer.

FEATURES source

1. 736
 /organism="Picea glauca"
 /mol_type="mRNA"
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 /db_xref="taxon:3330"
 /clone="GQ0085 M24"
 /sex="Hermaphrodite"
 /tissue_type="Vascular cambium, secondary phloem and bark
 of trees girdled by removing a ring of bark ca. 1 cm wide
 from the midpoint of the main stem"
 /dev_stage="Vascular cambium, secondary phloem, and bark
 from trees harvested 1 and 7 days after girdling
 treatment"
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 saplings"
 /note="Organ: Main stem of 4 year old saplings,
 approximately 60 cm tall; Vector: pBluescript II SK (+)
 XR; Site 1: Eco-RI; Site 2: Xho-I; Tissues were pooled
 from above and below the girdle. cDNA was prepared from 5
 mg of poly A+ selected RNA and was directionally ligated
 into the pBluescript II SK (+) XR vector (Stratagene),
 transformed by electroporation into DH10B cells (in
 vitrogen) for propagation"

ORIGIN

Query Match 72.4%; Score 535.2; DB 7; Length 736;
 Best Local Similarity 94.8%; Pred. No. 7.1e-157;
 Matches 565; Conservative 0; Mismatches 28; Indels 3; Gaps 1;
 121 AGTGAGACTTTTCAACAAAGGTAATATCGGGAACCTCTCGGATTCATTCGCCAGCT 180
 40 ATTGAGACTTTTCAACAAAGGTAATATCGGGAACCTCTCGGATTCATTCGCCAGCT 99
 181 ATCTGTCACTTCATCAAAAGGACAGTAGAAGGAAGGTGGCACCTACAAATGCCATCAT 240
 100 ATCTGTCACTTTATTGTGAAGATAGTGGAAAGGAAGGTGGCTCTCTACAAATGCCATCAT 159
 241 TGGCATAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAGATGGA 300
 160 TGGCATAAGAAAGGCGCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAGATGGA 219
 301 CCCCCACCCAGGAGCATCGTGGAAAAAGAACAGCGTTCCACACGCTCTTCAAAAGCAA 360
 220 CCCCCACCCAGGAGCATCGTGGAAAAAGAACAGCGTTCCACACGCTCTTCAAAAGCAA 279
 361 GTGGATTGATGTATTG---CAGTGAGACTTTTCAACAAAGGGTAATATCGGGAACCTC 417
 280 GTGGATTGATGTATTGTCGGATTGAGACTTTTCAACAAAGGGTAATATCGGGAACCTC 339
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 340 CTCGGATTCCATTGCCCGAGTATCTGTCATCTTCAATCTTGTGAAGATAGTGGAAAGGAAGGT 399
 478 GGCACTTACAATGCGCATTCATTGCGATAAGGAAGGCTATCGTTCAAGATGCCTCTGCC 537
 400 GGCTCTTACAATGCCATCATTTGCGATAAGGAAGGCGCATCGTTGAAGATGCCTCTGCC 459
 538 GACAGTGGTCCCAAGATGGACCCCAACCCAGGAGCATCGTGGAAAAAGGAAGACGTT 597

Db 460 GACAGTGGTCCCAAGATGGACCCCAACCCAGGAGCATCGTGGAAAAAGACGTT 519
 Qy 598 CCACCAACGCTCTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGAC 657
 Db 520 CCACCAACGCTCTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGAC 579
 Qy 658 GCACAAATCCCACTATCTTCGCAAGACCCCTCTCTATATAAGGAAGTTCATTTC 713
 Db 580 GCACAAATCCCACTATCTTCGCAAGACCCCTCTCTATATAAGGAAGTTCATTTC 635

RESULT 9

CK438348

LOCUS

DEFINITION

Picea glauca cDNA clone GQ0085_D16 5', mRNA sequence.

CK438348

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CK438348 698 bp mRNA linear EST 08-JAN-2004
 GQ0085_BR_D16 GQ008: Cambium, phloem and bark of girdled saplings
 Picea glauca cDNA clone GQ0085_D16 5', mRNA sequence.
 CK438348
 CK438348.1 GI:40769405
 EST.
 Picea glauca (white spruce)
 Picea glauca
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
 1 (bases 1 to 698)
 Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
 Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
 Siddiqui,A., Holt,R., Marra,M. and Mackay,J.
 Arborea EST sequencing in Picea glauca (white spruce)
 Unpublished (2004)
 Centre de Recherche en Biologie Forestiere
 Contact: John Mackay
 Universite Laval
 Pavillon Charles-Eugene Marchand, Quebec, Canada G1K 7P4
 Fax: 418 656 7493
 Email: jmackay@rsvs.ulaval.ca
 Center for Computational Genomics and Bioinformatics (CCGB),
 University of Minnesota, MN id Identifier: MN5174387 Clone ID:
 GQ0085 D16 Clones available through: John Mackay, Ph. D. Professeur
 adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
 de Recherche en Biologie Forestiere (Forest Biology Research
 Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
 Plate: 5 row: 16 column: D
 Seq primer: M13 Reverse Primer.

FEATURES

source

1. 638
 /organism="Picea glauca"
 /mol_type="mRNA"
 /strain="pg-653"
 /db_xref="taxon:3330"
 /clone="GQ0085 D16"
 /sex="Hermaphrodite"
 /tissue_type="Vascular cambium, secondary phloem and bark
 of trees girdled by removing a ring of bark ca. 1 cm wide
 from the midpoint of the main stem"
 /dev_stage="Vascular cambium, secondary phloem, and bark
 from trees harvested 1 and 7 days after girdling
 treatment"
 /lab_host="E. coli DH10B cells"
 /clone_lib="GQ008: Cambium, phloem and bark of girdled
 saplings"
 /note="Organ: Main stem of 4 year old saplings,
 approximately 60 cm tall; Vector: pBluescript II SK (+)
 XR; Site 1: Eco-RI; Site 2: Xho-I; Tissues were pooled
 from above and below the girdle. cDNA was prepared from 5
 mg of poly A+ selected RNA and was directionally ligated
 into the pBluescript II SK (+) XR vector (Stratagene),
 transformed by electroporation into DH10B cells (in
 vitrogen) for propagation"

ORIGIN

Query Match 72.4%; Score 533.2; DB 7; Length 698;
 Best Local Similarity 94.5%; Pred. No. 3e-156;

DEFINITION mgxb0003F18f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0003F18f, genomic survey sequence.

ACCESSION AQ362115

VERSION AQ362115.1 GI:4211034

KEYWORDS GSS.

SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)

ORGANISM Magnaporthe grisea

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 839)

AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M., Wang, R.A. and Dean, R.A.

TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome

JOURNAL Unpublished (1998)

COMMENT Contact: Dean RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson University, Clemson, SC 29634

Tel: 864 656 5737

Fax: 864 656 4293

Email: rdean@clemson.edu

Seq primer: TAATACGACTCACTATAGG

Class: BAC ends

High quality sequence start: 58

High quality sequence stop: 454.

Location/Qualifiers

FEATURES

source

1..839

/organism="Magnaporthe grisea"

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/strain="70-15"

/db_xref="taxon:148305"

/clones="mgxb0003F18f"

/tissue_type="Protoplasts"

/lab_host="E. coli DH10B"

/clone_lib="CUGI Rice Blast BAC Library"

/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII; Rice blast is one of the most devastating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

ORIGIN

Query Match 47.8%; Score 351.8; DB 8; Length 839;

Best Local Similarity 99.4%; Pred. No. 4.1e-99;

Matches 353; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

379 AGTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATTCGCCAGCT 438

163 ATTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATTCGCCAGCT 222

439 ATCTGTCACTTCATCAAAAGGACAGTAGAAGGAGGTGGCAGCTCAAAATGCCATCAT 498

223 ATCTGTCACTTCATCAAAAGGACAGTAGAAGGAGGTGGCAGCTCAAAATGCCATCAT 282

499 TGGGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCGGACAGTGGTCCCAAGATGGA 558

283 TGGGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCGGACAGTGGTCCCAAGATGGA 342

559 CCCCCACACGAGGAGCATCGTGAAAAGAGAGAGCTTCAACAGCATCTTCAAGGAA 618

343 CCCCCACACGAGGAGCATCGTGAAAAGAGAGAGCTTCAACAGCATCTTCAAGGAA 402

619 GTGGATTGATGTGATATCTCCACTGACGTAGGAGGATGACGACAAATCCCCTCTTCG 678

403 GTGGATTGATGTGATATCTCCACTGACGTAGGAGGATGACGACAAATCCCCTCTTCG 462

Qy 679 CAAGACCCCTTCTCTATATTAAGGAAGTTCAATTTGGAGAGACACGCTGGA 733

Db 463 CAAGACCCCTTCTCTATATTAAGGAAGTTCAATTTGGAGAGACACGCTGGA 517

RESULT 12

CG206846/c

LOCUS

DEFINITION

CG206846 654 bp DNA linear GSS 21-AUG-2003

TOS0467 TAMU Rice Japonica Nipponbare BAC Library (Hind III) Oryza

sativa (japonica cultivar-group) genomic clone TOSJNBh019110h,

genomic survey sequence.

ACCESSION CG206846

VERSION CG206846.1 GI:34097907

KEYWORDS GSS.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 654)

AUTHORS Li, Y., Wu, C., Santos, T., Uhm, T., Liu, D. and Zhang, H.-B.

TITLE BAC end sequences to close the gaps of a rice physical map at TAMU

JOURNAL Unpublished (2003)

COMMENT Contact: Wu C

Department of Soil and Crop Sciences and Institute for Plant

Genomics and Biotechnology

Texas A & M University

TAMU 2474, College Station, TX 77843-2474, USA

Tel: 979 862 4800

Fax: 979 862 4790

Email: c-wu@neo.tamu.edu

Seq primer: M13 universal Forward GTAAACACGCGCCAGT

Class: BAC ends

High quality sequence stop: 654.

Location/Qualifiers

FEATURES

source

1..654

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/cultivar="Nipponbare"

/db_xref="taxon:39947"

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/clone_lib="TAMU Rice Japonica Nipponbare BAC Library

(Hind III)"

/note="Vector: V41"

ORIGIN

Query Match 46.3%; Score 341; DB 9; Length 654;

Best Local Similarity 97.2%; Pred. No. 9.4e-96;

Matches 347; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

379 AGTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATTCGCCAGCT 438

524 ATTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATTCGCCAGCT 465

439 ATCTGTCACTTCATCAAAAGGACAGTAGAAGGAGGTGGCAGCTCAAAATGCCATCAT 498

464 ATCTGTCACTTCATCAAAAGGACAGTAGAAGGAGGTGGCAGCTCAAAATGCCATCAT 405

499 TGGGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCGGACAGTGGTCCCAAGATGGA 558

404 TGGGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCGGACAGTGGTCCCAAGATGGA 345

559 CCCCCACACGAGGAGCATCGTGAAAAGAGAGAGCTTCAACAGCATCTTCAAGGAA 618

344 CCCCCACACGAGGAGCATCGTGAAAAGAGAGAGCTTCAACAGCATCTTCAAGGAA 285

619 GTGGATTGATGTGATATCTCCACTGACGTAGGAGGATGACGACAAATCCCCTCTTCG 678

284 GTGGATTGATGTGATATCTCCACTGACGTAGGAGGATGACGACAAATCCCCTCTTCG 225

679 CAAGACCCCTTCTCTATATTAAGGAAGTTCAATTTGGAGAGACACGCTGATC 735


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||||| 331 ATCTGTCACTTTATTTGGAAGATAGTGAAAGGAGGTGGCTCCTCAAAATGCCATCAT 272
||||| 499 TGCATAAAGAAAGGCTATCGTTCAAGATCGCTCTGCCGACAGTGGTCCCAAGATGGA 558
||||| 271 TGCATAAAGAAAGGCTATCGTTGAAGATCGCTCTGCCGACAGTGGTCCCAAGATGGA 212
||||| 559 CCCCACCCACGAGGAGCATCGTGGAAAGAAAGACAGTTCACACAGTCTTCAAGCAA 618
||||| 211 CCCCACCCACGAGGAGCATCGTGGAAAGAAAGACAGTTCACACAGTCTTCAAGCAA 152
||||| 619 GTGATTTGATGTGATATCTCCACTGACGTAGGAGTACGACACAAATCCCCTATCCTTCG 678
||||| 151 GTGATTTGATGTGATATCTCCACTGACGTAGGAGTACGACACAAATCCCCTATCCTTCG 92
||||| 679 CAAGACCCCTTCTCTATATAGGAAGTTCATTTTCAATTGGAGAGGACACGCTGAA 733
||||| 91 CAAGACCCCTTCTCTATATAGGAAGTTCATTTTCAATTGGAGAGGACACGCTGAA 37

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RESULT 15
CG804983/c
LOCUS      1118056A07.y1 1118 - RescueMu Grid S Zea mays genomic, genomic
DEFINITION 469 bp DNA linear GSS 10-NOV-2003
survey sequence.
ACCESSION  CG804983
VERSION    CG804983.1 GI:38240957
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 469)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site found so sequence was trimmed.
Post-ligation sequence submitted separately.
Plate: 1118056 row: 40
Class: transposon-tagged.
Location/Qualifiers
1..469
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/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid S was grown at San Diego in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

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FEATURES

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source
1..469
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/lab_host="DH10B"
/clone_lib="1118 - RescueMu Grid S"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid S was grown at San Diego in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

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ORIGIN

Query Match 45.2%; Score 332.6; DB 9; Length 469;

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Best Local Similarity 96.1%; Pred. No. 3.7e-93;
Matches 341; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 379 AGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCCTATGCCCAGCT 438
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DB 390 ATTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCCTATGCCCAGCT 331
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QY 439 ATCTGTCACTTTCATCAAAAAGGACAGTAGAAAAGAGGAGGTGGCACCTTCAAAATGCCATCAT 498
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DB 330 ATCTGTCACTTTCATCAAAAAGGAGTAGTGAAGAGTGGTGGTCTCTACAAATGCCATCAT 271
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QY 499 TGCATAAAGAAAGGCTATCGTTCAAGATCGCTCTGCCGACAGTGGTCCCAAGATGGA 558
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DB 270 TGCATAAAGAAAGGCTATCGTTGAAGATGGCTCTGCCGACAGTGGTCCCAAGATGGA 211
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QY 559 CCCCACCCACGAGGAGCATCGTGGAAAGAAAGACAGTTCACACAGCTCTTCAAAAGCAA 618
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DB 210 CCCCACCCACGAGGAGCATCGTGGAAAGAAAGACAGTTCACACAGCTCTTCAAAAGCAA 151
|||||
QY 619 GTGATTTGATGTGATATCTCCACTGACGTAGGAGTACGACACAAATCCCCTATCCTTCG 678
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DB 150 GTGATTTGATGTGATATCTCCACTGACGTAGGAGTACGACACAAATCCCCTATCCTTCG 91
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QY 679 CAAGACCCCTTCTCTATATAGGAAGTTCATTTTCAATTGGAGAGGACACGCTGAA 733
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DB 90 CAAGACCCCTTCTCTATATAGGAAGTTCATTTTCAATTGGAGAGGACACGCTGAA 36
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Job time : 3219 secs

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